

Applicant
Copy
09/689,366
2/18/04

RESULT 2
PCT-US96-12860-5
Sequence 5, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08,512,946 & 08,569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-5

Query Match 100.0%; Score 307; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 4.9e-37;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDNRYKCCGGLMDNKLGDSP 55
DB 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDNRYKCCGGLMDNKLGDSP 55

RESULT 3
US-08-511-485-8
Sequence 8, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-8

Query Match 100.0%; Score 307; DB 2; Length 618;
Best Local Similarity 100.0%; Pred. No. 9.1e-36;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDNRYKCCGGLMDNKLGDSP 55
DB 45 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDNRYKCCGGLMDNKLGDSP 99

RESULT 4
US-09-212-971-8
Sequence 8, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K.
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-8

Query Match 100.0%; Score 307; DB 3; Length 618;
Best Local Similarity 100.0%; Pred. No. 9.1e-36;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDNRYKCCGGLMDNKLGDSP 55
DB 45 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDNRYKCCGGLMDNKLGDSP 99

RESULT 5
US-08-800-929A-8

Applicant Copy
09/689,366
2/18/2004

RESULT 2
PCT-US96-12860-7
Sequence 7, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBRACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-7

Query Match
Best Local Similarity 100.0%; Score 269; DB 5; Length 46;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRDDAMSEHRRHFPNCPF 46
DB 1 LARAGFYIIGPDRVACFACGKLSNWEPRDDAMSEHRRHFPNCPF 46

RESULT 3
US-08-511-485-23
Sequence 23, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-23

Query Match
Best Local Similarity 100.0%; Score 269; DB 2; Length 67;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRDDAMSEHRRHFPNCPF 46
DB 21 LARAGFYIIGPDRVACFACGKLSNWEPRDDAMSEHRRHFPNCPF 66

RESULT 4
PCT-US95-05922A-2
Sequence 2, Application PC/TUS9505922A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILLILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922A
FILING DATE: 11 MAY 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-292
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-05922A-2

Tue May 6 18:23:47 2003

US-08-569-749-2.ra1

09/689, 366 2/18/04
Examined Search Page 1
Notes

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 42.0069 Seconds
(without alignments)
432.865 Million cell updates/sec

Title: US-08-569-749-2
Perfect score: 3277
Sequence: 1 MHKTSQRLEPGSPSYQNIKS.....LNKPCICGIIKGTIRFLS 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3277	100.0	618	4	US-08-569-749-2
2	3277	100.0	618	4	US-09-069-023-29
3	3277	100.0	618	5	PCIT-US96-12860-2
4	3247	99.1	618	2	US-08-511-485-8
5	3247	99.1	618	3	US-09-212-971-8
6	3247	99.1	618	4	US-08-800-929A-8
7	3247	99.1	618	4	US-09-617-053A-8
8	2728	83.2	612	4	US-08-569-749-14
9	2728	83.2	612	5	PCIT-US96-12860-14
10	2724	83.1	612	3	US-09-212-971-14
11	2724	83.1	612	4	US-08-800-929A-14
12	2724	83.1	612	4	US-09-617-053A-14
13	2353	71.8	604	4	US-08-569-749-4
14	2353	71.8	604	5	PCIT-US96-12860-4
15	2332	71.2	604	2	US-08-511-485-6
16	2332	71.2	604	3	US-09-212-971-6
17	2332	71.2	604	4	US-08-800-929A-6
18	2326	71.0	604	4	US-09-617-053A-6
19	2326	71.0	600	5	PCIT-US96-05922A-2
20	2172	66.3	600	3	US-09-212-971-12
21	2172	66.3	600	4	US-08-800-929A-12
22	2172	66.3	600	4	US-09-617-053A-12
23	909	27.7	497	2	US-08-511-485-4
24	909	27.7	497	3	US-09-212-971-4
25	909	27.7	497	4	US-08-800-929A-4
26	909	27.7	497	4	US-09-617-053A-4
27	874	26.7	496	2	US-08-511-485-10

28	874	26.7	496	3	US-09-212-971-10	Sequence 10, Appl
29	874	26.7	496	4	US-08-800-929A-10	Sequence 10, Appl
30	874	26.7	496	4	US-09-617-053A-10	Sequence 10, Appl
31	736.5	22.5	498	2	US-08-511-485-13	Sequence 13, Appl
32	513	15.7	268	3	US-08-836-134-22	Sequence 22, Appl
33	513	15.7	268	4	US-09-493-784-22	Sequence 22, Appl
34	492.5	15.0	236	4	US-09-239-867-4	Sequence 4, Appl
35	463	14.1	1151	3	US-08-836-134-23	Sequence 23, Appl
36	463	14.1	1151	4	US-09-493-784-23	Sequence 23, Appl
37	463	14.1	1232	3	US-08-836-134-2	Sequence 2, Appl
38	463	14.1	1232	4	US-09-493-784-2	Sequence 2, Appl
39	461	14.1	275	2	US-08-511-485-12	Sequence 12, Appl
40	461	14.1	275	3	US-08-836-134-21	Sequence 21, Appl
41	461	14.1	275	4	US-09-493-784-21	Sequence 21, Appl
42	458.5	14.0	236	4	US-09-121-979-4	Sequence 4, Appl
43	458.5	14.0	236	4	US-09-332-319-4	Sequence 4, Appl
44	458.5	14.0	236	4	US-09-239-867-2	Sequence 2, Appl
45	431	13.2	89	4	US-09-099-041A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-569-749-2
Sequence 2, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-2
Query Match 100.0%; Score 3277; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 3.4e-308;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHKTSQRLEPGSPSYQNIKSIMEDSTILSDWTNSNOKMKYDFSCELYRSTYEPAGV 60
DB 1 MHKTSQRLEPGSPSYQNIKSIMEDSTILSDWTNSNOKMKYDFSCELYRSTYEPAGV 60
QY 61 PVSEKSLARAGFYITGVNDKVCFCGLMDLNWKLGDSPLOKHKOLYPPSCFIONLVAS 120

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Db 61 PVSERSLARAGFYIYGVNDKYKFCFCGLMDNMKLGDSPIQKHQLYPSCSFIONLVAS 120
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Db 121 LGSTSKNTSPMRNSFAHSLSPLEHSSLSFGSYSSLSPNPLNSRAVEDISSRTNPYSYA 180
QY 181 MSTEERFLTYHMPDLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEPRKDDAMSEH 240
Db 181 MSTEERFLTYHMPDLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEPRKDDAMSEH 240
QY 241 RRHFPNCPFLNSLETFLRSISNLSMOTHAARMRTFMYPSSVPVQPEQLASAGFYVGR 300
Db 241 RRHFPNCPFLNSLETFLRSISNLSMOTHAARMRTFMYPSSVPVQPEQLASAGFYVGR 300
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Db 301 NDDVKCFCCDGLRCWESGDDPWYEHAKWPRCEFLIRKKGQEFVDEIQRYPHLEQL 360
QY 361 STSDTTGEENADPPIIHFGGESSSEDAVMANTPVKSALEMGNRDLVKQVQSKILTT 420
Db 361 STSDTTGEENADPPIIHFGGESSSEDAVMANTPVKSALEMGNRDLVKQVQSKILTT 420
QY 421 GENYKTVNDIVSALLNAEDEKREBEKEKQAEEMASDDSLIRKRNMLFOQLTCVLPILD 480
Db 421 GENYKTVNDIVSALLNAEDEKREBEKEKQAEEMASDDSLIRKRNMLFOQLTCVLPILD 480
QY 481 NLKNAVINKOEHDIIKQTOIPQARELIDTILYKGNAAANIFKNCKEIDSTLYKNLF 540
Db 481 NLKNAVINKOEHDIIKQTOIPQARELIDTILYKGNAAANIFKNCKEIDSTLYKNLF 540
QY 541 VDKNMKIPTEDVSGLSLEQLRLQEBERTCKVCMDEKESVVFIPCGHLVVOCECAPSLR 600
Db 541 VDKNMKIPTEDVSGLSLEQLRLQEBERTCKVCMDEKESVVFIPCGHLVVOCECAPSLR 600
QY 601 KCPICRGIINGTVRTFLS 618
Db 601 KCPICRGIINGTVRTFLS 618

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RESULT 2

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US-09-069-023-29
; Sequence 29, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: US-03333
; CURRENT APPLICATION NUMBER: US/09/069, 023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-29

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Query Match 100.0%; Score 3277; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 3.4e-308;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PVSERSLARAGFYIYGVNDKYKFCFCGLMDNMKLGDSPIQKHQLYPSCSFIONLVAS 120
Db 61 PVSERSLARAGFYIYGVNDKYKFCFCGLMDNMKLGDSPIQKHQLYPSCSFIONLVAS 120

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QY 121 LGSTSKNTSPMRNSFAHSLSPLEHSSLSFGSYSSLSPNPLNSRAVEDISSRTNPYSYA 180
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Db 181 MSTEERFLTYHMPDLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEPRKDDAMSEH 240
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Db 301 NDDVKCFCCDGLRCWESGDDPWYEHAKWPRCEFLIRKKGQEFVDEIQRYPHLEQL 360
QY 361 STSDTTGEENADPPIIHFGGESSSEDAVMANTPVKSALEMGNRDLVKQVQSKILTT 420
Db 361 STSDTTGEENADPPIIHFGGESSSEDAVMANTPVKSALEMGNRDLVKQVQSKILTT 420
QY 421 GENYKTVNDIVSALLNAEDEKREBEKEKQAEEMASDDSLIRKRNMLFOQLTCVLPILD 480
Db 421 GENYKTVNDIVSALLNAEDEKREBEKEKQAEEMASDDSLIRKRNMLFOQLTCVLPILD 480
QY 481 NLKNAVINKOEHDIIKQTOIPQARELIDTILYKGNAAANIFKNCKEIDSTLYKNLF 540
Db 481 NLKNAVINKOEHDIIKQTOIPQARELIDTILYKGNAAANIFKNCKEIDSTLYKNLF 540
QY 541 VDKNMKIPTEDVSGLSLEQLRLQEBERTCKVCMDEKESVVFIPCGHLVVOCECAPSLR 600
Db 541 VDKNMKIPTEDVSGLSLEQLRLQEBERTCKVCMDEKESVVFIPCGHLVVOCECAPSLR 600
QY 601 KCPICRGIINGTVRTFLS 618
Db 601 KCPICRGIINGTVRTFLS 618

```

RESULT 3

PCT-US96-12860-2

Sequence 2, Application PC/TUS9612860

GENERAL INFORMATION:

APPLICANT: TULARIK, INC.

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/12860

FILING DATE: 06 AUG 1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)781-1989

TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 618 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-2

Query Match 100.0%; Score 3277; DB 5; Length 618;
Best local Similarity 100.0%; Pred. No. 3.4e-308;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHKTASQRLFPGPSYONIKSIMEDSTILSDWTNSNKKMKYDFSCELYRMSTYSPAGV 60
DB 1 MHKTASQRLFPGPSYONIKSIMEDSTILSDWTNSNKKMKYDFSCELYRMSTYSPAGV 60
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DB 121 LGSTSKNTSPMRNSFAHSLSPTEHSSLSFGSYSSLSPPNPLNSRAVEDISSRTNPSYA 180
QY 181 MSTERARFLTYHMPFLTFLSPSELARAGFYTYGPDRAVACFACGCKLSNWEPKDAMSEH 240
DB 181 MSTERARFLTYHMPFLTFLSPSELARAGFYTYGPDRAVACFACGCKLSNWEPKDAMSEH 240
QY 241 RHRPNCPLFENSLFETLFRSISNLSMOTHAARMRTFMYWPSVVPQPEQLASAGFYTYGR 300
DB 241 RHRPNCPLFENSLFETLFRSISNLSMOTHAARMRTFMYWPSVVPQPEQLASAGFYTYGR 300
QY 301 NDDVYKCFCCDGLRCWESGDDPVVEHAKWPRCEFLIRMKGOEFVDEIOGRYPHLEQL 360
DB 301 NDDVYKCFCCDGLRCWESGDDPVVEHAKWPRCEFLIRMKGOEFVDEIOGRYPHLEQL 360
QY 361 STSDTGEENADPPIIHFGPGESESDAVMMNTPVYKSALEGFNDLVKQTVQSKILTT 420
DB 361 STSDTGEENADPPIIHFGPGESESDAVMMNTPVYKSALEGFNDLVKQTVQSKILTT 420
QY 421 GENYKTVNDIVSALLNAEDEKREKEKQAEEMASDLSLRKNRMAFFOQLTCVLPILD 480
DB 421 GENYKTVNDIVSALLNAEDEKREKEKQAEEMASDLSLRKNRMAFFOQLTCVLPILD 480
QY 481 NLKANVINKQEHDIKQTOIPLQARLIDITLVKGNAAANIFKNCKEIDSTLYKNLF 540
DB 481 NLKANVINKQEHDIKQTOIPLQARLIDITLVKGNAAANIFKNCKEIDSTLYKNLF 540
QY 541 VDKNMKIYPTEDVSGLSLEQLRLQERTCKVCMDEKESVVFIPCGHLVVCQECAPSLR 600
DB 541 VDKNMKIYPTEDVSGLSLEQLRLQERTCKVCMDEKESVVFIPCGHLVVCQECAPSLR 600
QY 601 KCPICRGIIKGTVRTFLS 618
DB 601 KCPICRGIIKGTVRTFLS 618

RESULT 4
US-08-511-485-8
Sequence 8, Application US/08511485
Patent No. 5919912

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511.485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-8

Query Match 99.1%; Score 3247; DB 2; Length 618;
Best local Similarity 99.4%; Pred. No. 2.7e-305;
Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHKTASQRLFPGPSYONIKSIMEDSTILSDWTNSNKKMKYDFSCELYRMSTYSPAGV 60
DB 1 MHKTASQRLFPGPSYONIKSIMEDSTILSDWTNSNKKMKYDFSCELYRMSTYSPAGV 60
QY 61 PVSESLARAGFYTYGVNDKVKFCGCGMLDMNKLGDSPICQKHQOLYPCSCFTQNLVSAS 120
DB 61 PVSESLARAGFYTYGVNDKVKFCGCGMLDMNKLGDSPICQKHQOLYPCSCFTQNLVSAS 120
QY 121 LGSTSKNTSPMRNSFAHSLSPTEHSSLSFGSYSSLSPPNPLNSRAVEDISSRTNPSYA 180
DB 121 LGSTSKNTSPMRNSFAHSLSPTEHSSLSFGSYSSLSPPNPLNSRAVEDISSRTNPSYA 180
QY 181 MSTERARFLTYHMPFLTFLSPSELARAGFYTYGPDRAVACFACGCKLSNWEPKDAMSEH 240
DB 181 MSTERARFLTYHMPFLTFLSPSELARAGFYTYGPDRAVACFACGCKLSNWEPKDAMSEH 240
QY 241 RHRPNCPLFENSLFETLFRSISNLSMOTHAARMRTFMYWPSVVPQPEQLASAGFYTYGR 300
DB 241 RHRPNCPLFENSLFETLFRSISNLSMOTHAARMRTFMYWPSVVPQPEQLASAGFYTYGR 300
QY 301 NDDVYKCFCCDGLRCWESGDDPVVEHAKWPRCEFLIRMKGOEFVDEIOGRYPHLEQL 360
DB 301 NDDVYKCFCCDGLRCWESGDDPVVEHAKWPRCEFLIRMKGOEFVDEIOGRYPHLEQL 360
QY 361 STSDTGEENADPPIIHFGPGESESDAVMMNTPVYKSALEGFNDLVKQTVQSKILTT 420
DB 361 STSDTGEENADPPIIHFGPGESESDAVMMNTPVYKSALEGFNDLVKQTVQSKILTT 420
QY 421 GENYKTVNDIVSALLNAEDEKREKEKQAEEMASDLSLRKNRMAFFOQLTCVLPILD 480
DB 421 GENYKTVNDIVSALLNAEDEKREKEKQAEEMASDLSLRKNRMAFFOQLTCVLPILD 480
QY 481 NLKANVINKQEHDIKQTOIPLQARLIDITLVKGNAAANIFKNCKEIDSTLYKNLF 540
DB 481 NLKANVINKQEHDIKQTOIPLQARLIDITLVKGNAAANIFKNCKEIDSTLYKNLF 540
QY 541 VDKNMKIYPTEDVSGLSLEQLRLQERTCKVCMDEKESVVFIPCGHLVVCQECAPSLR 600
DB 541 VDKNMKIYPTEDVSGLSLEQLRLQERTCKVCMDEKESVVFIPCGHLVVCQECAPSLR 600
QY 601 KCPICRGIIKGTVRTFLS 618
DB 601 KCPICRGIIKGTVRTFLS 618

RESULT 5
US-09-212-971-8Sequence 8, Application US/09212971B
Patent No. 6107041

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-8

Query Match 99.1%; Score 3247; DB 3; Length 618;
Best Local Similarity 99.4%; Pred. No. 2.7e-305;
Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHKTASQRLPPGSPSYONIKSIMEDSTILSDWTNSNKKOKKYDFSCELYRMSTYSTEPAGV 60
DB 1 MHKTASQRLPPGSPSYONIKSIMEDSTILSDWTNSNKKOKKYDFSCELYRMSTYSTEPAGV 60
QY 61 PVSERSLARAGFYTGVDNKKVCCGGLMDNWKLGDSPIQKHQOLYPCSFIONLYSAS 120
DB 61 PVSERSLARAGFYTGVDNKKVCCGGLMDNWKLGDSPIQKHQOLYPCSFIONLYSAS 120
QY 121 LGSTSKMTSPMRNSFAHSLSTLEHSSLSFGSYSLSPNPLNSRAVEDISSRTNPSYA 180
DB 121 LGSTSKMTSPMRNSFAHSLSTLEHSSLSFGSYSLSPNPLNSRAVEDISSRTNPSYA 180
QY 181 MSTEERAFLLTYHMPPLTFLSPSELARAGFYIGPDRVACFACGGLKSNWEPKDDAMSEH 240
DB 181 MSTEERAFLLTYHMPPLTFLSPSELARAGFYIGPDRVACFACGGLKSNWEPKDDAMSEH 240
QY 241 RRHFPNCPFLNLSLETLRFSTSNLSMOTHAARMRTFMWPSVVPQPEGLASAGFYVGR 300
DB 241 RRHFPNCPFLNLSLETLRFSTSNLSMOTHAARMRTFMWPSVVPQPEGLASAGFYVGR 300
QY 301 NDDVKCCCGDGLRCWESGDDPWVHAKEWPRCEFLIRKKGQEVDEIOGRYPHLEQL 360
DB 301 NDDVKCCCGDGLRCWESGDDPWVHAKEWPRCEFLIRKKGQEVDEIOGRYPHLEQL 360
QY 361 STSDTTEENADPPIIHFGPESSSEDAVMNTPVKSALEMJFNBDLVKQTVOSKILTT 420
DB 361 STSDTTEENADPPIIHFGPESSSEDAVMNTPVKSALEMJFNBDLVKQTVOSKILTT 420
QY 421 GENYKTYNDIYSALLNAEDEKREKEKQAEEMASDDLIRKRMALFQQLCVLPILD 480
DB 421 GENYKTYNDIYSALLNAEDEKREKEKQAEEMASDDLIRKRMALFQQLCVLPILD 480
QY 481 NLKANVINKQEHDIKQKQIPIQARELIDTILVKGNAANIFKNCLEKIDSTLYKNLF 540
DB 481 NLKANVINKQEHDIKQKQIPIQARELIDTILVKGNAANIFKNCLEKIDSTLYKNLF 540

QY 541 VDKNMKYPEDVSGLSLEBQRLQOERTCKYCMKREVSVPFPCGHLVYQOECAPSLR 600
DB 541 VDKNMKYPEDVSGLSLEBQRLQOERTCKYCMKREVSVPFPCGHLVYQOECAPSLR 600
QY 601 KPCICRGIKGTVPRTFLS 618
DB 601 KPCICRGIKGTVPRTFLS 618

RESULT 6
US-08-800-929A-8Sequence 8, Application US/08800929A
Patent No. 6133437

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
DISEASE
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elding LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOSSOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354

FILING DATE: 26-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045

TELEX:

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-800-929A-8

Query Match 99.1%; Score 3247; DB 4; Length 618;
Best Local Similarity 99.4%; Pred. No. 2.7e-305;
Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHKTASQRLPPGSPSYONIKSIMEDSTILSDWTNSNKKOKKYDFSCELYRMSTYSTEPAGV 60
DB 1 MHKTASQRLPPGSPSYONIKSIMEDSTILSDWTNSNKKOKKYDFSCELYRMSTYSTEPAGV 60
QY 61 PVSERSLARAGFYTGVDNKKVCCGGLMDNWKLGDSPIQKHQOLYPCSFIONLYSAS 120
DB 61 PVSERSLARAGFYTGVDNKKVCCGGLMDNWKLGDSPIQKHQOLYPCSFIONLYSAS 120

QY 121 LGSTKNTSPMRNSFAHSLSPTEHSSLPFGSSLSLSPNPLNRAVEDISSRTNPSYA 180
DB 121 LGSTKNTSPMRNSFAHSLSPTEHSSLPFGSSLSLSPNPLNRAVEDISSRTNPSYA 180
QY 181 MSTEARFLTYHMMPLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEPRKDANSEH 240
DB 181 MSTEARFLTYHMMPLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEPRKDANSEH 240
QY 241 RRHFPNCPFLSNSLTFLRFSISNLSMOTHAARMRTFMYPSSVVPVQPOLASAGFYVGR 300
DB 241 RRHFPNCPFLSNSLTFLRFSISNLSMOTHAARMRTFMYPSSVVPVQPOLASAGFYVGR 300
QY 301 NDDVKCFCCDGLRCWESGDDPWVEHAKWPPRCEFLIRKKGQEFVDEIOGRYPHLLBOLL 360
DB 301 NDDVKCFCCDGLRCWESGDDPWVEHAKWPPRCEFLIRKKGQEFVDEIOGRYPHLLBOLL 360
QY 361 STSDTTGEENADPPIIHFGGESSSEDVAMNTPVYKSALEMGNRDLVKQTVQSKILTT 420
DB 361 STSDTTGEENADPPIIHFGGESSSEDVAMNTPVYKSALEMGNRDLVKQTVQSKILTT 420
QY 421 GENYKTVDIVSALINAEDEREKEKQAEEMASDDLILIRKNRMALFOQLTCVLPILD 480
DB 421 GENYKTVDIVSALINAEDEREKEKQAEEMASDDLILIRKNRMALFOQLTCVLPILD 480
QY 481 NLKANVINKEOHDIIKQTOIPLQARELIDTILYKGNAAANIFKNCLKEIDSTLYKNLF 540
DB 481 NLKANVINKEOHDIIKQTOIPLQARELIDTILYKGNAAANIFKNCLKEIDSTLYKNLF 540
QY 541 VDKNMKYIPTEDVSGSLERQLRQOEERTCKVCMDEKSVVFIIPCGHLVYQECAPSLR 600
DB 541 VDKNMKYIPTEDVSGSLERQLRQOEERTCKVCMDEKSVVFIIPCGHLVYQECAPSLR 600
QY 601 KCPICRGIIKGTVRTFLS 618
DB 601 KCPICRGIIKGTVRTFLS 618

RESULT 7
US-09-617-053A-8
; Sequence 8, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-617-053A-8

Query Match 99.1%; Score 3247; DB 4; Length 618;
Best Local Similarity 99.4%; Pred. No. 2,7e-305;
Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHKTASORLFPGPSYONIKSIMEDSTILSDMTNSNKKMKYDPSCELYRMSTYSTFPAGV 60
DB 1 MHKTASORLFPGPSYONIKSIMEDSTILSDMTNSNKKMKYDPSCELYRMSTYSTFPAGV 60

QY 61 PVSESLARAGFYTYGVNDKVCFCGGLMLDNWKLGDSPIOKHQOLYPSCSFTUNLVAS 120
DB 61 PVSESLARAGFYTYGVNDKVCFCGGLMLDNWKLGDSPIOKHQOLYPSCSFTUNLVAS 120
QY 121 LGSTKNTSPMRNSFAHSLSPTEHSSLPFGSSLSLSPNPLNRAVEDISSRTNPSYA 180
DB 121 LGSTKNTSPMRNSFAHSLSPTEHSSLPFGSSLSLSPNPLNRAVEDISSRTNPSYA 180
QY 181 MSTEARFLTYHMMPLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEPRKDANSEH 240
DB 181 MSTEARFLTYHMMPLTFLSPSELARAGFYIIGPDRAVACFACGKLSNWEPRKDANSEH 240
QY 241 RRHFPNCPFLSNSLTFLRFSISNLSMOTHAARMRTFMYPSSVVPVQPOLASAGFYVGR 300
DB 241 RRHFPNCPFLSNSLTFLRFSISNLSMOTHAARMRTFMYPSSVVPVQPOLASAGFYVGR 300
QY 301 NDDVKCFCCDGLRCWESGDDPWVEHAKWPPRCEFLIRKKGQEFVDEIOGRYPHLLBOLL 360
DB 301 NDDVKCFCCDGLRCWESGDDPWVEHAKWPPRCEFLIRKKGQEFVDEIOGRYPHLLBOLL 360
QY 361 STSDTTGEENADPPIIHFGGESSSEDVAMNTPVYKSALEMGNRDLVKQTVQSKILTT 420
DB 361 STSDTTGEENADPPIIHFGGESSSEDVAMNTPVYKSALEMGNRDLVKQTVQSKILTT 420
QY 421 GENYKTVDIVSALINAEDEREKEKQAEEMASDDLILIRKNRMALFOQLTCVLPILD 480
DB 421 GENYKTVDIVSALINAEDEREKEKQAEEMASDDLILIRKNRMALFOQLTCVLPILD 480
QY 481 NLKANVINKEOHDIIKQTOIPLQARELIDTILYKGNAAANIFKNCLKEIDSTLYKNLF 540
DB 481 NLKANVINKEOHDIIKQTOIPLQARELIDTILYKGNAAANIFKNCLKEIDSTLYKNLF 540
QY 541 VDKNMKYIPTEDVSGSLERQLRQOEERTCKVCMDEKSVVFIIPCGHLVYQECAPSLR 600
DB 541 VDKNMKYIPTEDVSGSLERQLRQOEERTCKVCMDEKSVVFIIPCGHLVYQECAPSLR 600
QY 601 KCPICRGIIKGTVRTFLS 618
DB 601 KCPICRGIIKGTVRTFLS 618

RESULT 8
US-08-569-749-14
; Sequence 14, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Goeddel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,749
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-14

Query Match 83.2%; Score 2728; DB 4; Length 612;
Best Local Similarity 83.4%; Pred. No. 4.5e-25;
Matches 517; Conservative 45; Mismatches 48; Indels 10; Gaps 6;

QY 1 MHKASQRLFPSPSYONIKSIMEDSTILSDWTNSNKKQKDYDECELYRMSTYSTFPAGY 60
1 MDTKVSQRLGQGLHOKLRIMEKSTILSNWTKSEKKKDFCELYRMSTYSTSAFPRGY 60
DB 1 MDTKVSQRLGQGLHOKLRIMEKSTILSNWTKSEKKKDFCELYRMSTYSTSAFPRGY 60
QY 61 PVSESLARAGFYTTGVNDKVCFCGGLMDNMKLGDSPIQKHQOLYPCSFQIONLYSAS 120
61 PVSESLARAGFYTTGVNDKVCFCGGLMDNMKLGDSPIQKHQOLYPCSFQIONLYSAS 120
DB 61 PVSESLARAGFYTTGVNDKVCFCGGLMDNMKLGDSPIQKHQOLYPCSFQIONLYSAS 120
QY 121 LGSTSKNTSPMRNSFAHSLPTLEHSSLSFGSSYSLSPNPLNSRAVEDISSRTNPSYA 180
121 LGSTSKNTSPMRNSFAHSLPTLEHSSLSFGSSYSLSPNPLNSRAVEDISSRTNPSYA 180
DB 121 LGSTSKNTSPMRNSFAHSLPTLEHSSLSFGSSYSLSPNPLNSRAVEDISSRTNPSYA 180
QY 181 MSTEARFLTYHMPPLTFLSPBELARAGFYIIGPDVACACGKLSNWEPRKDAMSEH 240
174 MSTEARFLTYHMPPLTFLSPBELARAGFYIIGPDVACACGKLSNWEPRKDAMSEH 240
DB 174 MSTEARFLTYHMPPLTFLSPBELARAGFYIIGPDVACACGKLSNWEPRKDAMSEH 240
QY 241 RRHFPNCPFLNLETLRFISINLSMOTHAARMRTFMWPSVPVQPEOLASAGFYVGR 300
241 RRHFPNCPFLNLETLRFISINLSMOTHAARMRTFMWPSVPVQPEOLASAGFYVGR 300
DB 241 RRHFPNCPFLNLETLRFISINLSMOTHAARMRTFMWPSVPVQPEOLASAGFYVGR 300
QY 294 NDDVKCFCCDGLRCWESGDDPWVEHAKWPRCEFLIRMKGOEFVDEIOGRYPHLEQL 360
294 NDDVKCFCCDGLRCWESGDDPWVEHAKWPRCEFLIRMKGOEFVDEIOGRYPHLEQL 360
DB 294 NDDVKCFCCDGLRCWESGDDPWVEHAKWPRCEFLIRMKGOEFVDEIOGRYPHLEQL 360
QY 361 STSDTGEENADP--PIIHFGESSESDAVMMNTPVYKSALEMGFNRLDYKQVOSKIL 418
361 STSDTGEENADP--PIIHFGESSESDAVMMNTPVYKSALEMGFNRLDYKQVOSKIL 418
DB 361 STSDTGEENADP--PIIHFGESSESDAVMMNTPVYKSALEMGFNRLDYKQVOSKIL 418
QY 419 TTGENYKTVNDIVSALINAEDEREKREKQAEASDLSLRKNRMALFOQLTCLVPI 478
419 TTGENYKTVNDIVSALINAEDEREKREKQAEASDLSLRKNRMALFOQLTCLVPI 478
DB 419 TTGENYKTVNDIVSALINAEDEREKREKQAEASDLSLRKNRMALFOQLTCLVPI 478
QY 479 LDNLKANVINKQEHDIKQTOIPLQARELIDTLVKGNAANIFKNCLEIDSTLYKN 538
479 LDNLKANVINKQEHDIKQTOIPLQARELIDTLVKGNAANIFKNCLEIDSTLYKN 538
DB 479 LDNLKANVINKQEHDIKQTOIPLQARELIDTLVKGNAANIFKNCLEIDSTLYKN 538
QY 539 LFVDKNNKIPTEDVSGLSLEQLRLQERTCKYCMDEKVSVPVIFPCGHLVYCOECAPS 598
539 LFVDKNNKIPTEDVSGLSLEQLRLQERTCKYCMDEKVSVPVIFPCGHLVYCOECAPS 598
DB 539 LFVDKNNKIPTEDVSGLSLEQLRLQERTCKYCMDEKVSVPVIFPCGHLVYCOECAPS 598
QY 599 LRKCPICGIIKGTVRTFLS 618
599 LRKCPICGIIKGTVRTFLS 618
DB 599 LRKCPICGIIKGTVRTFLS 618

RESULT 9

PCT-US96-12860-14
Sequence 14, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-14

Query Match 83.2%; Score 2728; DB 5; Length 612;
Best Local Similarity 83.4%; Pred. No. 4.5e-25;
Matches 517; Conservative 45; Mismatches 48; Indels 10; Gaps 6;

QY 1 MHKASQRLFPSPSYONIKSIMEDSTILSDWTNSNKKQKDYDECELYRMSTYSTFPAGY 60
1 MDTKVSQRLGQGLHOKLRIMEKSTILSNWTKSEKKKDFCELYRMSTYSTSAFPRGY 60
DB 1 MDTKVSQRLGQGLHOKLRIMEKSTILSNWTKSEKKKDFCELYRMSTYSTSAFPRGY 60
QY 61 PVSESLARAGFYTTGVNDKVCFCGGLMDNMKLGDSPIQKHQOLYPCSFQIONLYSAS 120
61 PVSESLARAGFYTTGVNDKVCFCGGLMDNMKLGDSPIQKHQOLYPCSFQIONLYSAS 120
DB 61 PVSESLARAGFYTTGVNDKVCFCGGLMDNMKLGDSPIQKHQOLYPCSFQIONLYSAS 120
QY 121 LGSTSKNTSPMRNSFAHSLPTLEHSSLSFGSSYSLSPNPLNSRAVEDISSRTNPSYA 180
121 LGSTSKNTSPMRNSFAHSLPTLEHSSLSFGSSYSLSPNPLNSRAVEDISSRTNPSYA 180
DB 121 LGSTSKNTSPMRNSFAHSLPTLEHSSLSFGSSYSLSPNPLNSRAVEDISSRTNPSYA 180
QY 181 MSTEARFLTYHMPPLTFLSPBELARAGFYIIGPDVACACGKLSNWEPRKDAMSEH 240
174 MSTEARFLTYHMPPLTFLSPBELARAGFYIIGPDVACACGKLSNWEPRKDAMSEH 240
DB 174 MSTEARFLTYHMPPLTFLSPBELARAGFYIIGPDVACACGKLSNWEPRKDAMSEH 240
QY 241 RRHFPNCPFLNLETLRFISINLSMOTHAARMRTFMWPSVPVQPEOLASAGFYVGR 300
241 RRHFPNCPFLNLETLRFISINLSMOTHAARMRTFMWPSVPVQPEOLASAGFYVGR 300
DB 241 RRHFPNCPFLNLETLRFISINLSMOTHAARMRTFMWPSVPVQPEOLASAGFYVGR 300
QY 294 NDDVKCFCCDGLRCWESGDDPWVEHAKWPRCEFLIRMKGOEFVDEIOGRYPHLEQL 360
294 NDDVKCFCCDGLRCWESGDDPWVEHAKWPRCEFLIRMKGOEFVDEIOGRYPHLEQL 360
DB 294 NDDVKCFCCDGLRCWESGDDPWVEHAKWPRCEFLIRMKGOEFVDEIOGRYPHLEQL 360
QY 361 STSDTGEENADP--PIIHFGESSESDAVMMNTPVYKSALEMGFNRLDYKQVOSKIL 418
361 STSDTGEENADP--PIIHFGESSESDAVMMNTPVYKSALEMGFNRLDYKQVOSKIL 418
DB 361 STSDTGEENADP--PIIHFGESSESDAVMMNTPVYKSALEMGFNRLDYKQVOSKIL 418
QY 419 TTGENYKTVNDIVSALINAEDEREKREKQAEASDLSLRKNRMALFOQLTCLVPI 478
419 TTGENYKTVNDIVSALINAEDEREKREKQAEASDLSLRKNRMALFOQLTCLVPI 478
DB 419 TTGENYKTVNDIVSALINAEDEREKREKQAEASDLSLRKNRMALFOQLTCLVPI 478
QY 479 LDNLKANVINKQEHDIKQTOIPLQARELIDTLVKGNAANIFKNCLEIDSTLYKN 538
479 LDNLKANVINKQEHDIKQTOIPLQARELIDTLVKGNAANIFKNCLEIDSTLYKN 538
DB 479 LDNLKANVINKQEHDIKQTOIPLQARELIDTLVKGNAANIFKNCLEIDSTLYKN 538
QY 539 LFVDKNNKIPTEDVSGLSLEQLRLQERTCKYCMDEKVSVPVIFPCGHLVYCOECAPS 598
539 LFVDKNNKIPTEDVSGLSLEQLRLQERTCKYCMDEKVSVPVIFPCGHLVYCOECAPS 598
DB 539 LFVDKNNKIPTEDVSGLSLEQLRLQERTCKYCMDEKVSVPVIFPCGHLVYCOECAPS 598
QY 599 LRKCPICGIIKGTVRTFLS 618
599 LRKCPICGIIKGTVRTFLS 618
DB 599 LRKCPICGIIKGTVRTFLS 618

Db 593 LKCPICRGITKGTVTFLS 612

RESULT 10
US-09-212-971-14
; Sequence 14, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212, 971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017, 354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030, 590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800, 929
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-212-971-14

Query Match 83.1%; Score 2724; DB 3; Length 612;
Best Local Similarity 83.2%; Pred. No. 1.1e-254;
Matches 516; Conservative 46; Mismatches 48; Indels 10; Gaps 6;

QY 1 MHKTAQRLFPGPSYONIKSIMEDSTIISDWTNSNKKMKYDFSCELYRMSTYSPAGV 60
1 MUKTVSQRLOGGTLHOKLRIMEKSTILSNWTKSEKKKFDSCELYRMSTYSAFPGV 60
Db 1 MUKTVSQRLOGGTLHOKLRIMEKSTILSNWTKSEKKKFDSCELYRMSTYSAFPGV 60
QY 61 PVSESLARAGFYTGVDNDRKFCFCGGLMDNMKLGDSPIQKHQOLYPSCFIONLVAS 120
61 PVSESLARAGFYTGVDNDRKFCFCGGLMDNMKLGDSPIQKHQOLYPSCFIONLVAS 120
Db 61 PVSESLARAGFYTGVDNDRKFCFCGGLMDNMKLGDSPIQKHQOLYPSCFIONLVAS 120
QY 121 LGSTSKTSPARNSEHSLSTLEHSSLSFSGSYSLSPNPLNSRAVEDISSRTNPSYA 180
121 LGSTSKTSPARNSEHSLSTLEHSSLSFSGSYSLSPNPLNSRAVEDISSRTNPSYA 180
Db 121 LGSTSKTSPARNSEHSLSTLEHSSLSFSGSYSLSPNPLNSRAVEDISSRTNPSYA 180
QY 181 MSTEARFLTYHMPPLFLSPSELARAGFYIGPDRAVACFACGKLSNWEPRDDAMSEH 240
181 MSTEARFLTYHMPPLFLSPSELARAGFYIGPDRAVACFACGKLSNWEPRDDAMSEH 240
Db 181 MSTEARFLTYHMPPLFLSPSELARAGFYIGPDRAVACFACGKLSNWEPRDDAMSEH 240
QY 174 MSTEARFLTYHMPPLFLSPSELARAGFYIGPDRAVACFACGKLSNWEPRDDAMSEH 233
174 MSTEARFLTYHMPPLFLSPSELARAGFYIGPDRAVACFACGKLSNWEPRDDAMSEH 233
Db 174 MSTEARFLTYHMPPLFLSPSELARAGFYIGPDRAVACFACGKLSNWEPRDDAMSEH 233
QY 241 RHHFPCPLENLETLRFSTISNLSMOTHAARMRTFMWPSVVPQPEOLASAGFYVGR 300
241 RHHFPCPLENLETLRFSTISNLSMOTHAARMRTFMWPSVVPQPEOLASAGFYVGR 300
Db 241 RHHFPCPLENLETLRFSTISNLSMOTHAARMRTFMWPSVVPQPEOLASAGFYVGR 300
QY 234 RHHFPCPLENLETLRFSTISNLSMOTHAARMRTFMWPSVVPQPEOLASAGFYVGR 293
234 RHHFPCPLENLETLRFSTISNLSMOTHAARMRTFMWPSVVPQPEOLASAGFYVGR 293
Db 234 RHHFPCPLENLETLRFSTISNLSMOTHAARMRTFMWPSVVPQPEOLASAGFYVGR 293
QY 301 NDDVKCCCGDGLRCWESGDPVWEHAKWPRCEFLIRMKGEVDEIGRYHLLBOLL 360
301 NDDVKCCCGDGLRCWESGDPVWEHAKWPRCEFLIRMKGEVDEIGRYHLLBOLL 360
Db 301 NDDVKCCCGDGLRCWESGDPVWEHAKWPRCEFLIRMKGEVDEIGRYHLLBOLL 360
QY 294 NDDVKCCCGDGLRCWESGDPVWEHAKWPRCEFLIRMKGEVDEIGRYHLLBOLL 353
294 NDDVKCCCGDGLRCWESGDPVWEHAKWPRCEFLIRMKGEVDEIGRYHLLBOLL 353
Db 294 NDDVKCCCGDGLRCWESGDPVWEHAKWPRCEFLIRMKGEVDEIGRYHLLBOLL 353
QY 361 STSDTGEENADP-DIHFGPGESESDAVMMNTPVKSALENGFNRLVKQTVOSKIL 418
361 STSDTGEENADP-DIHFGPGESESDAVMMNTPVKSALENGFNRLVKQTVOSKIL 418
Db 361 STSDTGEENADP-DIHFGPGESESDAVMMNTPVKSALENGFNRLVKQTVOSKIL 418
QY 354 STSDTGEENADP-DIHFGPGESESDAVMMNTPVKSALENGFNRLVKQTVOSKIL 412
354 STSDTGEENADP-DIHFGPGESESDAVMMNTPVKSALENGFNRLVKQTVOSKIL 412
Db 354 STSDTGEENADP-DIHFGPGESESDAVMMNTPVKSALENGFNRLVKQTVOSKIL 412
QY 419 TIGENYKTVNDIVSALNAEDEKREKEKEKOEEMASDLSLRKNRMALFOOLTQVAPI 478
419 TIGENYKTVNDIVSALNAEDEKREKEKEKOEEMASDLSLRKNRMALFOOLTQVAPI 478
Db 419 TIGENYKTVNDIVSALNAEDEKREKEKEKOEEMASDLSLRKNRMALFOOLTQVAPI 478
QY 413 ATGENYKTVNDIVSALNAEDEKREKEKEKOEEMASDLSLRKNRMALFOOLTQVAPI 472
413 ATGENYKTVNDIVSALNAEDEKREKEKEKOEEMASDLSLRKNRMALFOOLTQVAPI 472
Db 413 ATGENYKTVNDIVSALNAEDEKREKEKEKOEEMASDLSLRKNRMALFOOLTQVAPI 472
QY 479 LNNLKRANVINKEOHEHIIKQTOIPLQARELIDITLVKGNAAANIFKNLKEIDSTLYKN 538
479 LNNLKRANVINKEOHEHIIKQTOIPLQARELIDITLVKGNAAANIFKNLKEIDSTLYKN 538
Db 479 LNNLKRANVINKEOHEHIIKQTOIPLQARELIDITLVKGNAAANIFKNLKEIDSTLYKN 538
QY 473 LNNLKRANVINKEOHEHIIKQTOIPLQARELIDITLVKGNAAANIFKNLKEIDSTLYKN 532
473 LNNLKRANVINKEOHEHIIKQTOIPLQARELIDITLVKGNAAANIFKNLKEIDSTLYKN 532
Db 473 LNNLKRANVINKEOHEHIIKQTOIPLQARELIDITLVKGNAAANIFKNLKEIDSTLYKN 532

QY 539 LFVDKMKYIPTEDVSGLSLEBQLRLQEBERTCKVCMDEKESVVFIPCGHLVVCQECAPS 598
539 LFVDKMKYIPTEDVSGLSLEBQLRLQEBERTCKVCMDEKESVVFIPCGHLVVCQECAPS 598
Db 539 LFVDKMKYIPTEDVSGLSLEBQLRLQEBERTCKVCMDEKESVVFIPCGHLVVCQECAPS 598
QY 599 LKCPICRGITKGTVTFLS 618
599 LKCPICRGITKGTVTFLS 618
Db 599 LKCPICRGITKGTVTFLS 612

RESULT 11
US-08-800-929A-14
; Sequence 14, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elding LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800, 929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030, 590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017, 354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 612 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-800-929A-14

Query Match 83.1%; Score 2724; DB 4; Length 612;
Best Local Similarity 83.2%; Pred. No. 1.1e-254;
Matches 516; Conservative 46; Mismatches 48; Indels 10; Gaps 6;

QY 1 MHKTAQRLFPGPSYONIKSIMEDSTIISDWTNSNKKMKYDFSCELYRMSTYSPAGV 60
1 MUKTVSQRLOGGTLHOKLRIMEKSTILSNWTKSEKKKFDSCELYRMSTYSAFPGV 60
Db 1 MUKTVSQRLOGGTLHOKLRIMEKSTILSNWTKSEKKKFDSCELYRMSTYSAFPGV 60
QY 61 PVSESLARAGFYTGVDNDRKFCFCGGLMDNMKLGDSPIQKHQOLYPSCFIONLVAS 120
61 PVSESLARAGFYTGVDNDRKFCFCGGLMDNMKLGDSPIQKHQOLYPSCFIONLVAS 120
Db 61 PVSESLARAGFYTGVDNDRKFCFCGGLMDNMKLGDSPIQKHQOLYPSCFIONLVAS 120

Db 61 PVSESLARAGFYTYGVNDKVKCFCCGLMDNMKQD:SPVEKHPFPSCSFVOTLLSAS 120
QY 121 LGSTSKNTSPMRNSFAHSLSPLEHSSLSFGSYSSLPNPLNSRAVEDISSRTNPSYA 180
Db 121 LQSPSKNSPVKSRFAHS-SP-LER---GGIHSNLCSSPLNSRAVEDF-SSRMDPCSYA 173
QY 181 MSTEARFLTYHMPPLFLSPSELARAGFYTYIGPDRAVACFACGKLSNWEPRKDAMSEH 240
Db 174 MSTEARFLTYHMPPLFLSPSELARAGFYTYIGPDRAVACFACGKLSNWEPRKDAMSEH 233
QY 241 RRHFPNCPLENSLETFLRSISNLSMOTHAARMFTMYPPSSVPVQPEOLASAGFYVGR 300
Db 234 RRHFPNCPLENSLETFLRSISNLSMOTHAARMFTMYPPSSVPVQPEOLASAGFYVDR 293
QY 301 NDDVKCFCCDGLRCWESGDDPWVEHAKWFPCEFLIRKKGQEFVDEIOARYPHLLEOLL 360
Db 294 NDDVKCFCCDGLRCWESGDDPWVEHAKWFPCEFLIRKKGQEFVDEIOARYPHLLEOLL 353
QY 361 STSDTGTGENADP--PIIHGPGESSSEDAVMANTPVKSALEMGFNRLVKOTVQSKIL 418
Db 354 STSDTGTGENADPTEFVVFHFGPE--SSKDVYMMSTPVKAALEMGSFSLVQTVQROIL 412
QY 419 TTGENYKTVNDIVSALINAEDEREKEKEKOEEMASDLSLRKNRMALFQOLTHVLPI 478
Db 413 ATGENYKTVNDIVSALINAEDEREKEKEKOEEMASDLSLRKNRMALFQOLTHVLPI 472
QY 479 LDNLKANVINKOEHDIIKQOIPLOARELIDTILVKGNAANIFKNCLKEIDSTLYKN 538
Db 473 LDNLKANVINKOEHDIIKQOIPLOARELIDTILVKGNAANIFKNCLKEIDSTLYKN 532
QY 539 LFVDKNMKYIPTEDVSGLSLEQLRLQOERTCKVCMDEVSVEIFPCGHLVVOCECAPS 598
Db 533 LFVDKNMKYIPTEDVSGLSLEQLRLQOERTCKVCMDEVSVEIFPCGHLVVOCECAPS 592
QY 599 LRKCPICRGITKGTVRTFLS 618
Db 593 LRKCPICRGITKGTVRTFLS 612

RESULT 12
US-09-617-053A-14
; Sequence 14, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-617-053A-14

Query Match 83.1%; Score 2724; DB 4; Length 612;
Best Local Similarity 83.2%; Pred. No. 1.1e-254;
Matches 516; Conservative 46; Mismatches 48; Indels 10; Gaps 6;

QY 1 MKHTASQRLFPGPSYONIKSIMEDSTILSDWTNSKQKMYDPSCELYRMSTYSTFPAGV 60
Db 1 MKHTASQRLFPGPSYONIKSIMEDSTILSDWTNSKQKMYDPSCELYRMSTYSTFPAGV 60

QY 61 PVSESLARAGFYTYGVNDKVKCFCCGLMDNMKLGSDSPLOKHQOLYPCSFOTLNVAS 120
Db 61 PVSESLARAGFYTYGVNDKVKCFCCGLMDNMKQD:SPVEKHPFPSCSFVOTLLSAS 120
QY 121 LGSTSKNTSPMRNSFAHSLSPLEHSSLSFGSYSSLPNPLNSRAVEDISSRTNPSYA 180
Db 121 LQSPSKNSPVKSRFAHS-SP-LER---GGIHSNLCSSPLNSRAVEDF-SSRMDPCSYA 173
QY 181 MSTEARFLTYHMPPLFLSPSELARAGFYTYIGPDRAVACFACGKLSNWEPRKDAMSEH 240
Db 174 MSTEARFLTYHMPPLFLSPSELARAGFYTYIGPDRAVACFACGKLSNWEPRKDAMSEH 233
QY 241 RRHFPNCPLENSLETFLRSISNLSMOTHAARMFTMYPPSSVPVQPEOLASAGFYVGR 300
Db 234 RRHFPNCPLENSLETFLRSISNLSMOTHAARMFTMYPPSSVPVQPEOLASAGFYVDR 293
QY 301 NDDVKCFCCDGLRCWESGDDPWVEHAKWFPCEFLIRKKGQEFVDEIOARYPHLLEOLL 360
Db 294 NDDVKCFCCDGLRCWESGDDPWVEHAKWFPCEFLIRKKGQEFVDEIOARYPHLLEOLL 353
QY 361 STSDTGTGENADP--PIIHGPGESSSEDAVMANTPVKSALEMGFNRLVKOTVQSKIL 418
Db 354 STSDTGTGENADPTEFVVFHFGPE--SSKDVYMMSTPVKAALEMGSFSLVQTVQROIL 412
QY 419 TTGENYKTVNDIVSALINAEDEREKEKEKOEEMASDLSLRKNRMALFQOLTHVLPI 478
Db 413 ATGENYKTVNDIVSALINAEDEREKEKEKOEEMASDLSLRKNRMALFQOLTHVLPI 472
QY 479 LDNLKANVINKOEHDIIKQOIPLOARELIDTILVKGNAANIFKNCLKEIDSTLYKN 538
Db 473 LDNLKANVINKOEHDIIKQOIPLOARELIDTILVKGNAANIFKNCLKEIDSTLYKN 532
QY 539 LFVDKNMKYIPTEDVSGLSLEQLRLQOERTCKVCMDEVSVEIFPCGHLVVOCECAPS 598
Db 533 LFVDKNMKYIPTEDVSGLSLEQLRLQOERTCKVCMDEVSVEIFPCGHLVVOCECAPS 592
QY 599 LRKCPICRGITKGTVRTFLS 618
Db 593 LRKCPICRGITKGTVRTFLS 612

RESULT 13
US-08-569-749-4
; Sequence 4, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rotne, Mike
; APPLICANT: Goeddel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/569,749
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Breznar, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989

TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-4

Query Match 71.8%; Score 2353; DB 4; Length 604;
Best Local Similarity 72.8%; Pred. No. 8.5e-219;
Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;

QY 20 SIMEDSTILSDWTNS-NKQMKYDFSCLEYRMSTYSTFPAGVYSESLARAGFYTGYN 78
DB 2 NIVENSIFLSNLMKSAFTPELKYDLSCLEYRMSTYSTFPAGVYSESLARAGFYTGYN 61
QY 79 DKVCCCGGLMDNKKLGDSPIQKHQLYPSCSFIONLVSA-SLGSTSKNTSP--MRNSF 135
DB 62 DKVCCCGGLMDNKKRGDSPTKHKLLPSCRFVQSLNVNLEATSQPTPPSSVTNS- 120
QY 136 AHSLSPTLEHSSLSFGSYSLSPNPLNSRAVEDISSRTNTPSYAMSTEARFLTYHMP 195
DB 121 THSLPBTENSGYFRGYSNSPSPVNSRANQDFSAIMKRSYHCAMNNENARLLTQYWP 180
QY 196 LTFLESPSELRAGFYIIGPDRAVCFACGGKLSNWEKPDAMSEHRRFPNCPFLNSL- 254
DB 181 LTFLESPDLAKAGFYIIGPDRAVCFACGGKLSNWEKPDAMSEHRRFPNCPFLNSLQ 240
QY 255 ETLRFSISNLSMOTHAARMTFTWPSVYVPEQLASAGFYVGRNDVKCFCCDGLR 314
DB 241 DTSRYTVSNLSMOTHAARMTFTWPSVYVPEQLASAGFYVGRNDVKCFCCDGLR 300
QY 315 CWESGDDPWVHAHAKWPRCEFLIRMKGFVDEIQRYPHLEQLLSTDTTGEENADPP 374
DB 301 CWESGDDPWVHAHAKWPRCEFLIRMKGFVDEIQRYPHLEQLLSTDTTGEENADPP 360
QY 375 IIFHGGESESDAVMNTPVVKSALFENGFRDLVKOTVQSKILTTGENYKTYNDISAL 434
DB 361 IIFHGGESESDAVMNTPVVKSALFENGFRDLVKOTVQSKILTTGENYKTYNDISAL 420
QY 435 LNAEDEKREERKEKQAEEMASDLSLRKNRMALFOQLTCVLPILDLNLLKANVINQOEH 494
DB 421 LNAEDEIRERERERATEEKESNDLLIRKNRMALFOHLCVLPILDSLLTAGIINEQEH 480
QY 495 IIRKQTOIPLQARELIDTILVKGNAANIFKNCLEIDSTLYKNLFYDKNMKYIPTEDVS 554
DB 481 VIKQKQTSIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLFYDKNMKYIPTEDVS 540
QY 555 GLSLEQLRLQREERTCKYCMDEKVSIVFPCGHLVYVCOEAPSLRKCPIGIIKTGR 614
DB 541 DLPEEQRLRLQREERTCKYCMDEKVSIVFPCGHLVYVCOEAPSLRKCPIGIIKTGR 600
QY 615 TFLS 618
DB 601 TFLS 604

RESULT 14
PCT-US96-12860-4

Sequence 4, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-4

Query Match 71.8%; Score 2353; DB 5; Length 604;
Best Local Similarity 72.8%; Pred. No. 8.5e-219;
Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;

QY 20 SIMEDSTILSDWTNS-NKQMKYDFSCLEYRMSTYSTFPAGVYSESLARAGFYTGYN 78
DB 2 NIVENSIFLSNLMKSAFTPELKYDLSCLEYRMSTYSTFPAGVYSESLARAGFYTGYN 61
QY 79 DKVCCCGGLMDNKKLGDSPIQKHQLYPSCSFIONLVSA-SLGSTSKNTSP--MRNSF 135
DB 62 DKVCCCGGLMDNKKRGDSPTKHKLLPSCRFVQSLNVNLEATSQPTPPSSVTNS- 120
QY 136 AHSLSPTLEHSSLSFGSYSLSPNPLNSRAVEDISSRTNTPSYAMSTEARFLTYHMP 195
DB 121 THSLPBTENSGYFRGYSNSPSPVNSRANQDFSAIMKRSYHCAMNNENARLLTQYWP 180
QY 196 LTFLESPSELRAGFYIIGPDRAVCFACGGKLSNWEKPDAMSEHRRFPNCPFLNSL- 254
DB 181 LTFLESPDLAKAGFYIIGPDRAVCFACGGKLSNWEKPDAMSEHRRFPNCPFLNSLQ 240
QY 255 ETLRFSISNLSMOTHAARMTFTWPSVYVPEQLASAGFYVGRNDVKCFCCDGLR 314
DB 241 DTSRYTVSNLSMOTHAARMTFTWPSVYVPEQLASAGFYVGRNDVKCFCCDGLR 300
QY 315 CWESGDDPWVHAHAKWPRCEFLIRMKGFVDEIQRYPHLEQLLSTDTTGEENADPP 374
DB 301 CWESGDDPWVHAHAKWPRCEFLIRMKGFVDEIQRYPHLEQLLSTDTTGEENADPP 360
QY 375 IIFHGGESESDAVMNTPVVKSALFENGFRDLVKOTVQSKILTTGENYKTYNDISAL 434
DB 361 IIFHGGESESDAVMNTPVVKSALFENGFRDLVKOTVQSKILTTGENYKTYNDISAL 420
QY 435 LNAEDEKREERKEKQAEEMASDLSLRKNRMALFOQLTCVLPILDLNLLKANVINQOEH 494
DB 421 LNAEDEIRERERERATEEKESNDLLIRKNRMALFOHLCVLPILDSLLTAGIINEQEH 480
QY 495 IIRKQTOIPLQARELIDTILVKGNAANIFKNCLEIDSTLYKNLFYDKNMKYIPTEDVS 554
DB 481 VIKQKQTSIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLFYDKNMKYIPTEDVS 540
QY 555 GLSLEQLRLQREERTCKYCMDEKVSIVFPCGHLVYVCOEAPSLRKCPIGIIKTGR 614
DB 541 DLPEEQRLRLQREERTCKYCMDEKVSIVFPCGHLVYVCOEAPSLRKCPIGIIKTGR 600
QY 615 TFLS 618

Db 601 TFLS 604

RESULT 15
US-08-511-485-6
Sequence 6, Application US/08511485
Patent No. 5919912

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 604 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: both

MOLECULE TYPE: protein

US-08-511-485-6

Query Match 71.28; Score 2332; DB 2: Length 604;
Best Local Similarity 72.18; Pred. No. 9.2e-217;
Matches 435; Conservative 72; Mismatches 93; Indels 4; Gaps 4;

QY 20 SIMEDSTILSDWTNS-NKQKMYDFSCCLYRMSTYSTFPAGVPSERSLARAGFYTGYN 78
Db 2 NIVENSIFLSNLMKSNMTEFKYDLSCELYRMSTYSTFPAGVPSERSLARAGFYTGYN 61
QY 79 DKVCCFCGMLDNMKGDSPIQKHQOLYPSCSFTQNLVSA-SLGSSTKNTSPMRNSFA- 136
Db 62 DKVCCFCGMLDNMKGDSPTKHKIKLYPSCRFVQSLNSVNMLEATSQPTFPSSVTHST 121
QY 137 HSLSPLEHSLFSGYSLSLSPNPLNSRAVEDISSKRTNPYSAMSTEARFLTYHMPPL 196
Db 122 HSLPFTENGSGYFRGYSNSPNPNNSRANQEFALMRSSYPCPMNNEVARLLTFQWPL 181
QY 197 TFLSPSELARAGFYITGPGDVACFACGKLSNNEPKDDAMSEHRRHFPNCPLENSL-E 255
Db 182 TFLSPDLARAGFYITGPGDVACFACGKLSNNEPKDDAMSEHRRHFPNCPLENSL-E 241
QY 256 TLFSTISNLSMOTHAARMRTFMVSPVQPEOLASAGFYTGNDVYKFCDCDGLRC 315
Db 242 TSRYTVSNLSMOTHAARMRTFMVSPVQPEOLASAGFYTGNDVYKFCDCDGLRC 301
QY 316 WESGDDPWVEHAKWPRCEFLIRMGQEFVDEIGRYPHLLLECLLSTSDTGTGENADPPI 375

Db 302 WESGDDPWVQAKWPRCEFLIRMGQEFIRQVQASYPHLLLECLLSTSDSPGDNMAESSI 361
QY 376 IHFGPESSSEDVAMNTPYVKSALFMGNRDLVQVQSKILTTGENYKYVNDIVSALL 435
Db 362 IHLEPEDHSEDALMNTPYVINAAYEMGFSRLVQVQKILATGENTRLVNDIVDLDL 421
QY 436 NADEKREEREKQAEEMASDDLILRKNMALFQULFCVLPITDNLKANVINKQEHDI 495
Db 422 NADELREEREERATEKESNDLLIRKNMALFQULFCVLPITDNLKANVINKQEHDI 481
QY 496 IKQTOIPLOARELIDTILYKGNMAANIFRNCLEKIDSILYKNI-FVDKMKYTPEDVSG 555
Db 482 IKQTOISLQARELIDTILYKGNMAATVFRNSLQEAVALYEHLEFVQODIKYTPEDVSD 541
QY 556 LSLERQRLQDERCKVCMDKEVSVFIPCGHLVQCECAPSLRKCPICRGIIKGTVRT 615
Db 542 LPVEQLRLRLEBERCKVCMDKEVSIVFTPCGHLVQCECAPSLRKCPICRGIIKGTVRT 601
QY 616 FLS 618
Db 602 FLS 604

Search completed: May 5, 2003, 16:09:08
Job time: 44.0069 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:50:57 ; Search time 121.749 Seconds

(without alignments)
676.383 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277
Sequence: 1 MHKTASQRLFPSPSYONIKS.....LKKPCICRGIIKGTVPFLS 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_101002:*

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
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15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3277	100.0	618	18	AAW19746 Human inhibitor of
2	3277	100.0	618	18	AAW13545 Human c-IAP1. Hom
3	3277	100.0	618	20	AAV33998 Human cellular inh
4	3247	99.1	618	18	AAW19583 Human apoptosis in
5	3247	99.1	618	19	AAW69296 Human HIAP-2 prote
6	3247	99.1	618	23	ABG56655 Human inhibitor of
7	2728	83.2	612	18	AAW13555 Murine c-IAP. Mus
8	2724	83.1	612	19	AAW69299 Murine HIAP-2 prot
9	2654	81.0	591	18	AAW19586 Mouse apoptosis in
10	2654	81.0	591	23	ABG56668 Mouse inhibitor of

11	2353	71.8	604	18	AAW19747	Human inhibitor of
12	2353	71.8	604	18	AAW13546	Human c-IAP2. Hom
13	2353	71.8	604	20	AAV52703	Human cellular inh
14	2353	71.8	604	20	AAV33997	Human cellular inh
15	2332	71.2	604	18	AAW19582	Human apoptosis in
16	2332	71.2	604	19	AAW69295	Human HIAP-1 prote
17	2332	71.2	604	23	ABG56664	Human inhibitor of
18	2326	71.0	438	17	AAW04583	Human inhibitor of
19	2172	66.3	600	19	AAW69298	Murine HIAP-1 prot
20	2152	65.7	602	23	ABG56667	Mouse apoptosis in
21	2148	65.5	602	18	AAW19585	Mouse inhibitor of
22	1678	51.2	1140	23	AAV97837	Human cysteine pro
23	1678	51.2	1141	22	AAW50694	Human APT-2-MT chl
24	1593	48.6	306	22	AAW02925	Angiotensin conver
25	910	27.8	496	18	AAW19745	Mouse inhibitor of
26	909	27.7	497	18	AAW19581	Human apoptosis in
27	909	27.7	497	19	AAW69294	Human XIAP protein
28	909	27.7	497	21	AAV99985	Human X-linked inh
29	909	27.7	497	23	ABG56663	Human inhibitor of
30	908	27.7	497	21	AAV59451	Human XIAP protein
31	874	26.7	496	18	AAW19584	Mouse apoptosis in
32	874	26.7	496	19	AAW69297	Murine XIAP protei
33	874	26.7	496	23	ABG56666	Mouse inhibitor of
34	760.5	23.2	464	23	AAU75747	Human inhibitor of
35	737.5	22.5	498	22	ABW62863	Drosophila melanog
36	735.5	22.4	498	18	AAW19748	Drosophila inhibit
37	539	16.4	108	22	AAE10158	Caspase recruitment
38	533.5	16.3	278	23	AAO20511	Protein of App rel
39	494	15.1	438	22	AAW48189	Drosophila mutant
40	490.5	15.0	438	22	AAW48190	Drosophila mutant
41	490	15.0	438	22	ABW67347	Drosophila melanog
42	490	15.0	438	22	ABW67347	Drosophila melanog
43	490	15.0	438	22	AAW48188	Drosophila wild-ty
44	490	15.0	438	22	AAW48192	Drosophila mutant
45	484	14.8	438	22	AAW48191	Drosophila mutant

ALIGNMENTS

RESULT 1	AAW19746	standard; Protein; 618 AA.
ID	AAW19746	
XX	AAW19746;	
AC	AAW19746;	
XX		
DT	16-SEP-1997	(first entry)
XX		
DE	Human inhibitor of apoptosis protein homologue MIH.	
XX		
KW	Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIH;	
KW	degenerative disease; infectious disease; autoimmune disease;	
KW	cancer; therapy; diagnosis.	
OS		
XX	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Region	46..113
FT	Region	/label= BIR
FT	Region	184..250
FT	Region	/label= BIR
FT	Region	269..337
FT	Region	/label= BIR
FT	Region	569..606
FT	Region	/label= RING_finger
PN	W09723501-A1.	
XX		
PD	03-JUL-1997.	
XX		
PF	20-DEC-1996;	96MO-AU00827.
XX		
PR	22-DEC-1995;	95AU-0007275.

Query	Match	Best Local Similarity	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
QY	1 MHKTASORLFPGPSYONKISIMEDSTILSDWTNSNKKMKYDSCETLRMSTYSTFPAGV 60	100.0%	3277	18	618	0	0	0	0	0
DB	1 MHKTASORLFPGPSYONKISIMEDSTILSDWTNSNKKMKYDSCETLRMSTYSTFPAGV 60	100.0%	3277	18	618	0	0	0	0	0
QY	61 PVSESLARAGFYTTGVNDKVCFCGGLMDNKKLGSPQIKKQLYPSCSFIONLVAS 120	100.0%	3277	18	618	0	0	0	0	0
DB	61 PVSESLARAGFYTTGVNDKVCFCGGLMDNKKLGSPQIKKQLYPSCSFIONLVAS 120	100.0%	3277	18	618	0	0	0	0	0
QY	121 LGSTSKTSPMNSFAHSLSPLEHSLFSGSYSLSPNPLNSRAVEDISSRTNPYSTA 180	100.0%	3277	18	618	0	0	0	0	0
DB	121 LGSTSKTSPMNSFAHSLSPLEHSLFSGSYSLSPNPLNSRAVEDISSRTNPYSTA 180	100.0%	3277	18	618	0	0	0	0	0
QY	181 MSTEEANFLTYHMPPLTFLLSPSELARAGFYITGPDRAVACFACGKLSNWEPRDDAMSEH 240	100.0%	3277	18	618	0	0	0	0	0
DB	181 MSTEEANFLTYHMPPLTFLLSPSELARAGFYITGPDRAVACFACGKLSNWEPRDDAMSEH 240	100.0%	3277	18	618	0	0	0	0	0
QY	241 RRHFPNCPFLSNSLETTLRFSISNLSMOTHAARMRTFMTPSSVVPQPOLASAGFYVYGR 300	100.0%	3277	18	618	0	0	0	0	0
DB	241 RRHFPNCPFLSNSLETTLRFSISNLSMOTHAARMRTFMTPSSVVPQPOLASAGFYVYGR 300	100.0%	3277	18	618	0	0	0	0	0
QY	301 NDDVKECCDGGGLRWESGDDPVEHAHAKFPRCEFLIRMGKGEVDEIQGRYPHLLLEQL 360	100.0%	3277	18	618	0	0	0	0	0
DB	301 NDDVKECCDGGGLRWESGDDPVEHAHAKFPRCEFLIRMGKGEVDEIQGRYPHLLLEQL 360	100.0%	3277	18	618	0	0	0	0	0
QY	361 STSDTTEENADPPIIHFGPGESSSEDAVMAMTPVVKALAEKMFNRDLVKQTVOSKILTT 420	100.0%	3277	18	618	0	0	0	0	0
DB	361 STSDTTEENADPPIIHFGPGESSSEDAVMAMTPVVKALAEKMFNRDLVKQTVOSKILTT 420	100.0%	3277	18	618	0	0	0	0	0
QY	421 GENYKYVNDIVSALLNADEKREKEKQAEEMASDDISLIRNRMALFOQLTCVLPILD 480	100.0%	3277	18	618	0	0	0	0	0
DB	421 GENYKYVNDIVSALLNADEKREKEKQAEEMASDDISLIRNRMALFOQLTCVLPILD 480	100.0%	3277	18	618	0	0	0	0	0
QY	481 NLKANVINKOEHDIIKOKTQIPLQARELIDTILVKGNAANAFKNCLEIDSTLYKNLF 540	100.0%	3277	18	618	0	0	0	0	0
DB	481 NLKANVINKOEHDIIKOKTQIPLQARELIDTILVKGNAANAFKNCLEIDSTLYKNLF 540	100.0%	3277	18	618	0	0	0	0	0
QY	541 VDKNMKRTIPTYEDVSGLSLEQLRLQERTCKVCMDEKVSVEIFPCGHLVVCQCAPSLR 600	100.0%	3277	18	618	0	0	0	0	0
DB	541 VDKNMKRTIPTYEDVSGLSLEQLRLQERTCKVCMDEKVSVEIFPCGHLVVCQCAPSLR 600	100.0%	3277	18	618	0	0	0	0	0
QY	601 KCPICRGIIKGYVTFELS 618	100.0%	3277	18	618	0	0	0	0	0

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Db      601 KCPICRGIIKGFVRTFLS 618
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RESULT 2
AAW13545
ID      AAW13545 standard; Protein; 618 AA.
XX      AAW13545;
AC      AAW13545;
XX      22-JUL-1997 (first entry)
DT      Human c-IAP1.
XX      IAP; Inhibitor; apoptosis; RING finger domain; restinosis;
KW      myocardial infarction; nephritis; HIV.
OS      Homo sapiens.
XX      WO9706182-A1.
XX      20-FEB-1997.
PD      06-AUG-1996; 96WO-US12860.
PF      08-DEC-1995; 95US-0569749.
PR      08-AUG-1995; 95US-0512946.
XX      (TULA-) TULARIK INC.
XX      Goeddel DV, Rothe M;
PI      WPI; 1997-154209/14.
XX      N-PSDB; AAT61590.
DR      Nucleic acids encoding cellular inhibitor of apoptosis proteins -
PT      useful for apoptosis regulation in cells to reduce or increase
PT      apoptosis and for pharmacological screening
XX      Disclosure; Page 18-20; 35pp; English.
XX      The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
CC      AAT61590/T61591) comprise a series of defined structural domain
CC      repeats and/or a RING finger domain; in particular, at least two of
CC      a first domain repeat (AAW13547 or AAW13548), a second domain repeat
CC      (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
CC      and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
CC      sequences derived from these human genes.
CC      The nucleic acid is used for recombinant prodn. of human cellular
CC      inhibitor of apoptosis protein which modulates apoptosis
CC      regulation. The nucleic acids are useful in therapies where
CC      increased cell-specific apoptosis is desired, e.g. in restinosis,
CC      inflammatory disease states, myocardial infarction, glomerular
CC      nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC      They can also be used in conditions requiring a reduction in
CC      apoptosis.
XX      Sequence 618 AA:
QY      Query Match 100.0%; Score 3277; DB 18; Length 618;
Db      Best Local Similarity 100.0%; Pred. No. 1,4e-284;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY      1 MHKTASORLPFGPSYQNIKSIMEDSTILSDWTNSNKKQMKYDFSCELYRMSTYTFPAGV 60
      |||||||
QY      1 MHKTASORLPFGPSYQNIKSIMEDSTILSDWTNSNKKQMKYDFSCELYRMSTYTFPAGV 60
      |||||||
QY      61 PYSERSLARAGFYTTGVNDKVKCFCCGMLDNMKLIGDGPPIQKHQOLYSCSFIONLVAS 120
      |||||||
QY      61 PYSERSLARAGFYTTGVNDKVKCFCCGMLDNMKLIGDGPPIQKHQOLYSCSFIONLVAS 120
      |||||||
QY      121 LGSTSKTSPMKNSFASLSPTLEHSSLFSGSTSSLSFNPPLNSRAVEDISSKRTNPYSTA 180
      |||||||

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Db 121 LGSTSKNTSPMRNSFAHSLPTLHSSLSFGSYSLSPNPLNSRAVEDISSRTNPSYA 180
QY 181 MSTEEARFLTYHMPPLFLSPSELARAGFYIIGPGDRVACACGGKLSNNEPKDDAMSEH 240
    |||||||
Db 181 MSTEEARFLTYHMPPLFLSPSELARAGFYIIGPGDRVACACGGKLSNNEPKDDAMSEH 240
QY 241 RRHFPNCPFLNSLETFLRFSISNLSMOTHAARMRTFMWPSVPVQPEOLASAGFYVGR 300
    |||||||
Db 241 RRHFPNCPFLNSLETFLRFSISNLSMOTHAARMRTFMWPSVPVQPEOLASAGFYVGR 300
QY 301 NNDVYKFCFCCDGGLRWESGDDPWVEHAKWFPCEFLIRMGQEFVDEIQRYPHLEQL 360
    |||||||
Db 301 NNDVYKFCFCCDGGLRWESGDDPWVEHAKWFPCEFLIRMGQEFVDEIQRYPHLEQL 360
QY 361 STSDTGEENADPPIIHFGPGSSSEDVAMMNTPVYKSALEMGNLDVQTVOSKILTT 420
    |||||||
Db 361 STSDTGEENADPPIIHFGPGSSSEDVAMMNTPVYKSALEMGNLDVQTVOSKILTT 420
QY 421 GENYKTVNDIVSALLNADEKEEKEKQAEEMASDDLSTLRKNMALFOOLTQVLPILD 480
    |||||||
Db 421 GENYKTVNDIVSALLNADEKEEKEKQAEEMASDDLSTLRKNMALFOOLTQVLPILD 480
QY 481 NLKANVINKEHDIKQTOIPLQARELIDTILVKGNAANIFKNCLKEIDSTLYKNLF 540
    |||||||
Db 481 NLKANVINKEHDIKQTOIPLQARELIDTILVKGNAANIFKNCLKEIDSTLYKNLF 540
QY 541 VDKNMKYIPTEDVSGLSLEQLRRLQBERTCVKCMDEKESVVFICGHLVVCQECAPSIR 600
    |||||||
Db 541 VDKNMKYIPTEDVSGLSLEQLRRLQBERTCVKCMDEKESVVFICGHLVVCQECAPSIR 600
QY 601 KCPICRGIIKGYVTFPLS 618
    |||||||
Db 601 KCPICRGIIKGYVTFPLS 618

RESULT 3
ID AAY33998 standard; Protein; 618 AA.
XX AAY33998;
XX 26-NOV-1999 (first entry)
DT XX
DE Human cellular inhibitor of apoptosis-1 sequence.
XX
KW Cellular inhibitor of Apoptosis-1; antisense; diagnostic; therapeutic;
KW c-IAP-1; prophylaxis; infection; inflammation; tumor formation.
XX
OS Homo sapiens.
XX
PN US958772-A.
XX
PD 28-SEP-1999.
XX
PE 03-DEC-1998; 98US-0205204.
XX
PR 03-DEC-1998; 98US-0205204.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowser LM, Ackermann EJ;
XX
DR WPI; 1999-561047/47.
DR N-PSDB; AA222143.
XX
PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-1
XX useful for e.g. diagnostics, therapeutics, and as research reagents.
XX
PS Example 13; Columns 41-46; 32pp; English.
XX
CC The invention provides antisense compounds of 8-30 nucleotides that
CC inhibit the expression of human Cellular Inhibitor of Apoptosis-1
CC (c-IAP-1). The antisense compounds may be used for diagnostics,

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CC therapeutics (for modulating the expression of c-IAP-1), prophylaxis
CC (e.g. to prevent or delay infection, inflammation, or tumor formation),
CC as research reagents (e.g. to distinguish between members of a biological
CC pathway) and in kits. The present sequence represents the human cellular
CC inhibitor of apoptosis-1.
XX
SQ Sequence 618 AA;
Query Match 100.0%; Score 3277; DB 20; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.4e-284;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHKTAQORLEPGPSYONIKSIMESTLISDWTNSNKKMYDFSCELYRSTYS*EPAGV 60
    |||||||
Db 1 MHKTAQORLEPGPSYONIKSIMESTLISDWTNSNKKMYDFSCELYRSTYS*EPAGV 60
QY 61 PVSESLARAGFYITGVNDKVCFCGGLMDNWKLDSPIDKHKQLYPSCSFIONLVAS 120
    |||||||
Db 61 PVSESLARAGFYITGVNDKVCFCGGLMDNWKLDSPIDKHKQLYPSCSFIONLVAS 120
QY 121 LGSTSKNTSPMRNSFAHSLPTLHSSLSFGSYSLSPNPLNSRAVEDISSRTNPSYA 180
    |||||||
Db 121 LGSTSKNTSPMRNSFAHSLPTLHSSLSFGSYSLSPNPLNSRAVEDISSRTNPSYA 180
QY 181 MSTEEARFLTYHMPPLFLSPSELARAGFYIIGPGDRVACACGGKLSNNEPKDDAMSEH 240
    |||||||
Db 181 MSTEEARFLTYHMPPLFLSPSELARAGFYIIGPGDRVACACGGKLSNNEPKDDAMSEH 240
QY 241 RRHFPNCPFLNSLETFLRFSISNLSMOTHAARMRTFMWPSVPVQPEOLASAGFYVGR 300
    |||||||
Db 241 RRHFPNCPFLNSLETFLRFSISNLSMOTHAARMRTFMWPSVPVQPEOLASAGFYVGR 300
QY 301 NNDVYKFCFCCDGGLRWESGDDPWVEHAKWFPCEFLIRMGQEFVDEIQRYPHLEQL 360
    |||||||
Db 301 NNDVYKFCFCCDGGLRWESGDDPWVEHAKWFPCEFLIRMGQEFVDEIQRYPHLEQL 360
QY 361 STSDTGEENADPPIIHFGPGSSSEDVAMMNTPVYKSALEMGNLDVQTVOSKILTT 420
    |||||||
Db 361 STSDTGEENADPPIIHFGPGSSSEDVAMMNTPVYKSALEMGNLDVQTVOSKILTT 420
QY 421 GENYKTVNDIVSALLNADEKEEKEKQAEEMASDDLSTLRKNMALFOOLTQVLPILD 480
    |||||||
Db 421 GENYKTVNDIVSALLNADEKEEKEKQAEEMASDDLSTLRKNMALFOOLTQVLPILD 480
QY 481 NLKANVINKEHDIKQTOIPLQARELIDTILVKGNAANIFKNCLKEIDSTLYKNLF 540
    |||||||
Db 481 NLKANVINKEHDIKQTOIPLQARELIDTILVKGNAANIFKNCLKEIDSTLYKNLF 540
QY 541 VDKNMKYIPTEDVSGLSLEQLRRLQBERTCVKCMDEKESVVFICGHLVVCQECAPSIR 600
    |||||||
Db 541 VDKNMKYIPTEDVSGLSLEQLRRLQBERTCVKCMDEKESVVFICGHLVVCQECAPSIR 600
QY 601 KCPICRGIIKGYVTFPLS 618
    |||||||
Db 601 KCPICRGIIKGYVTFPLS 618

RESULT 4
ID AAW19583 standard; Protein; 618 AA.
XX AAW19583;
XX 02-SEP-1997 (first entry)
DT XX
DE Human apoptosis inhibitor HIAP-2.
XX
KW Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration;
KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
XX
OS Homo sapiens.

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XX Key Location/Qualifiers
FH Domain 46..113
FT Domain /label= BIR-1
FT Domain 184..250
FT Domain /label= BIR-2
FT Domain 269..336
FT Domain /label= BIR-3
FT Domain 560..605
FT Domain /label= Ring_zinc_finger
XX MO9706255-A2.
XX 20-FEB-1997.
XX 05-AUG-1996; 96WO-IB01022.
XX 22-DEC-1995; 95US-0576956.
XX 04-AUG-1995; 95US-0511485.
XX (UYOT-) UNIV OTTAWA.
XX PA
XX PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX DR MPI: 1997-154262/14.
XX DR N-PSDB; AAT70838.
XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
XX PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
XX PT of susceptibility to apoptotic disease
XX PS Claim 27; Page 75-77; 219pp; English.
XX CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
XX CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
XX CC are inhibitors of apoptosis (IAP) and which are characterised by
XX CC the presence of a ring zinc finger domain (see also AAW19587) and at
XX CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
XX CC The HIAP amino acid sequences were deduced from cDNA clones (AAT70837
XX CC and AAT70838) from a human liver library. IAP polypeptides can be
XX CC expressed in host cells (in vitro or in vivo) and used in methods
XX CC for treating diseases and disorders involving apoptosis, esp. in a
XX CC human diagnosed as HIV-positive or as having AIDS, a
XX CC neurodegenerative disease, a myelodysplastic syndrome or an
XX CC ischemic injury, selected from myocardial infarction, stroke,
XX CC reperfusion injury, or a toxin-induced liver disease.
XX SQ Sequence 618 AA;

Query Match 99.1%; Score 3247; DB 16; Length 618;
Best Local Similarity 99.4%; Pred. No. 6.8e-282;
Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 301 NDVYKCFCCDGGILRCWESGDDPWVEHAKMFPRCEFLIRMGQEFVDEIQGRPHLLQQL 360
DB 301 NDVYKCFCCDGGILRCWESGDDPWVEHAKMFPRCEFLIRMGQEFVDEIQGRPHLLQQL 360
QY 361 STSDTGEENADPPIIHFGPGESSEDAVMNTPVKSALEGENFDLVKQTVOSKILTT 420
DB 361 STSDTGEENADPPIIHFGPGESSEDAVMNTPVKSALEGENFDLVKQTVOSKILTT 420
QY 421 GENYKTVNDIVSALLNAEDEKREKEKQAEEMASDLSLIRKNRAALFQQLTCVPIILD 480
DB 421 GENYKTVNDIVSALLNAEDEKREKEKQAEEMASDLSLIRKNRAALFQQLTCVPIILD 480
QY 481 NLKANVINKQEHDIKQTOIPLQARELIDITLVKGNAAANIFKNCKLEIDSTLYKNLF 540
DB 481 NLKANVINKQEHDIKQTOIPLQARELIDITLVKGNAAANIFKNCKLEIDSTLYKNLF 540
QY 541 VDKNMKYPTEDEVSGLSLEQLRRLQERTCKVCMDEKVSVEIFPGHLVYQECAPSLR 600
DB 541 VDKNMKYPTEDEVSGLSLEQLRRLQERTCKVCMDEKVSVEIFPGHLVYQECAPSLR 600
QY 601 KCPICRGIIKGTVRTFLS 618
DB 601 KCPICRGIIKGTVRTFLS 618

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RESULT 5
AAW69296
ID AAW69296 standard; Protein; 618 AA.
XX AC AAW69296;
XX DT 13-NOV-1998 (first entry)
XX DE Human HIAP-2 protein.
XX KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
XX KW proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein.
XX OS Homo sapiens.
XX PN WO9835693-A2;
XX PD 20-AUG-1998;
XX PF 13-FEB-1998; 98WO-IB00781.
XX PR 13-FEB-1997; 97US-0800929.
XX PA (UYOT-) UNIV OTTAWA.
XX PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
XX PI Tsang B;
XX DR MPI: 1998-467164/40.
XX DR N-PSDB; AAV55040.
XX PT Inducing apoptosis in proliferative mammalian cells with inhibitor
XX PT of IAP or NAIP polypeptide - also methods for prognosis based on
XX PT presence of IAP and NAIP, specifically applied to cancers involving
XX PT p53 mutations
XX PS Disclosure: Fig 3; 147pp; English.
XX CC This sequence is the human HIAP-2 protein, which is a inhibitor of
XX CC apoptosis protein (IAP), and can be used in the method of the invention.
XX CC The method is for enhancing apoptosis in cells from a mammal with
XX CC proliferative disease by treatment with a compound that inhibits
XX CC biological activity of an IAP or NAIP polypeptide. The inhibitory
XX CC compounds are used to treat proliferative diseases, specially cancers of
XX CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
XX CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
XX CC rectum, cervix or endometrium, particularly to increase their sensitivity
XX CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are

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CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors.

XX Sequence 618 AA;

Query Match 99.1%; Score 3247; DB 19; Length 618;
 Best Local Similarity 99.4%; Pred. No. 6.8e-282;
 Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHKTSQRLFPSPSYQNIKSIDEDSTILSDWTNSNKKMKYDFSCEDLYRMSTYSPAGV 60
 DB 1 MHKTSQRLFPSPSYQNIKSIDEDSTILSDWTNSNKKMKYDFSCEDLYRMSTYSPAGV 60
 QY 61 PVSESLARAGFYTYGVNDKVKCCGIMLDNWKLGDSPIQKHQOLYPCSCFTQNLVSAS 120
 DB 61 PVSESLARAGFYTYGVNDKVKCCGIMLDNWKLGDSPIQKHQOLYPCSCFTQNLVSAS 120
 QY 121 LGSTSKNTSPMRNSFAHSLPTLEHSSLSFGSSYSLSPNPLNSRAVEDISSRTNYSYA 180
 DB 121 LGSTSKNTSPMRNSFAHSLPTLEHSSLSFGSSYSLSPNPLNSRAVEDISSRTNYSYA 180
 QY 181 MSTEARFLTYHMPFLTFLSPSELARAGFYTYGPDRAVACACGAGKLSNWEKXDMASEH 240
 DB 181 MSTEARFLTYHMPFLTFLSPSELARAGFYTYGPDRAVACACGAGKLSNWEKXDMASEH 240
 QY 241 RRHPNCPFLNSLETLRISINLSMOTHAARMRTFMWPSVVPVPEQLASAGFYTYVGR 300
 DB 241 RRHPNCPFLNSLETLRISINLSMOTHAARMRTFMWPSVVPVPEQLASAGFYTYVGR 300
 QY 301 NDDVYKCFCCDGLRCWESGDDPVVEHAKWFPCEFLIRMKGGEFVDEIQGRPHILEQL 360
 DB 301 NDDVYKCFCCDGLRCWESGDDPVVEHAKWFPCEFLIRMKGGEFVDEIQGRPHILEQL 360
 QY 361 STSDTGEENADPPIIHFGPGESESDAVMMNTPVKSALENGFNRLVKQTVQSKILTT 420
 DB 361 STSDTGEENADPPIIHFGPGESESDAVMMNTPVKSALENGFNRLVKQTVQSKILTT 420
 QY 421 GENKTVNDIVSALINAEDEKREBEKEKQAEEMASDLSLRKNRMAALFOQLTCVLPILD 480
 DB 421 GENKTVNDIVSALINAEDEKREBEKEKQAEEMASDLSLRKNRMAALFOQLTCVLPILD 480
 QY 481 NLLANVINKQEHDIKQTOPLQARELIDTILVKGNAANIFKNCKEIDSTLYKNLF 540
 DB 481 NLLANVINKQEHDIKQTOPLQARELIDTILVKGNAANIFKNCKEIDSTLYKNLF 540
 QY 541 VDKNMKYPTEDEVSGLSLEQLRLQEBRTCKVCMDEKESVYFIPGHLVYVQECAPSLR 600
 DB 541 VDKNMKYPTEDEVSGLSLEQLRLQEBRTCKVCMDEKESVYFIPGHLVYVQECAPSLR 600
 QY 601 KCPICRGITKGTAVTFLS 618
 DB 601 KCPICRGITKGTAVTFLS 618

RESULT 6

ABG65665 standard; Protein; 618 AA.

AC ABG65665;

XX 26-AUG-2002 (first entry)

DE Human inhibitor of apoptosis, HIA2.

KW Human; antisense; inhibitor of apoptosis; HIA1; HIA2; XIAP;

KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;

KW pancreatic cancer; embryonic development; viral pathogenesis;

KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;

KW lupus erythematosus; herpes virus infection; pox virus infection;

KW adenovirus infection; proliferative disease.

XX Homo sapiens.
 OS WO200226968-A2.
 PN 04-APR-2002.
 PD 27-SEP-2001; 2001WO-CA01379.
 PF 28-SEP-2000; 2000US-0672717.
 PR (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX korneluk RG, lacasse E, bald S, holcik M, young S;
 PI WPI: 2002-479562/51.
 DR N-PSDB: ABK93871.
 DR Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases
 XX Disclosure: Fig 3; 135pp; English.

The invention relates to an inhibitor of apoptosis (IAP) antisense
 nucleic acid (I) that inhibits IAP biological activity, regardless of
 length of the antisense nucleic acid, the IAP proteins may be mouse
 or human XIAP, HIA1 or HIA2. Also included are a pharmaceutical
 composition comprising a mammalian IAP antisense molecule and a method of
 enhancing apoptosis in a cell, comprising administering a negative
 regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 antisense inhibitor is useful for enhancing apoptosis in a cell in a
 mammal diagnosed with a proliferative disease. The method is useful for
 treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC protein sequence.

XX Sequence 618 AA;

Query Match 99.1%; Score 3247; DB 23; Length 618;
 Best Local Similarity 99.4%; Pred. No. 6.8e-282;
 Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHKTSQRLFPSPSYQNIKSIDEDSTILSDWTNSNKKMKYDFSCEDLYRMSTYSPAGV 60
 DB 1 MHKTSQRLFPSPSYQNIKSIDEDSTILSDWTNSNKKMKYDFSCEDLYRMSTYSPAGV 60
 QY 61 PVSESLARAGFYTYGVNDKVKCCGIMLDNWKLGDSPIQKHQOLYPCSCFTQNLVSAS 120
 DB 61 PVSESLARAGFYTYGVNDKVKCCGIMLDNWKLGDSPIQKHQOLYPCSCFTQNLVSAS 120
 QY 121 LGSTSKNTSPMRNSFAHSLPTLEHSSLSFGSSYSLSPNPLNSRAVEDISSRTNYSYA 180
 DB 121 LGSTSKNTSPMRNSFAHSLPTLEHSSLSFGSSYSLSPNPLNSRAVEDISSRTNYSYA 180
 QY 181 MSTEARFLTYHMPFLTFLSPSELARAGFYTYGPDRAVACACGAGKLSNWEKXDMASEH 240
 DB 181 MSTEARFLTYHMPFLTFLSPSELARAGFYTYGPDRAVACACGAGKLSNWEKXDMASEH 240
 QY 241 RRHPNCPFLNSLETLRISINLSMOTHAARMRTFMWPSVVPVPEQLASAGFYTYVGR 300
 DB 241 RRHPNCPFLNSLETLRISINLSMOTHAARMRTFMWPSVVPVPEQLASAGFYTYVGR 300
 QY 301 NDDVYKCFCCDGLRCWESGDDPVVEHAKWFPCEFLIRMKGGEFVDEIQGRPHILEQL 360
 DB 301 NDDVYKCFCCDGLRCWESGDDPVVEHAKWFPCEFLIRMKGGEFVDEIQGRPHILEQL 360

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OY 361 STSDTGEENADPPIIHFGPESSESDAVMMNTPVYKSALEMGFNRDLVQTVQSKILT 420
DB 361 STSDTGEENADPPIIHFGPESSESDAVMMNTPVYKSALEMGFNRDLVQTVQSKILT 420
OY 421 GENYKTVNDIVSALNAEDEKREERKEKQAEEMASDDLIRKNRMALFQQLCVLPILD 480
DB 421 GENYKTVNDIVSALNAEDEKREERKEKQAEEMASDDLIRKNRMALFQQLCVLPILD 480
OY 481 NLKANYINKQEHDIKQKQIPLQARELIDTILVKGNAANIRKNCKLEIDSTLYKNLF 540
DB 481 NLKANYINKQEHDIKQKQIPLQARELIDTILVKGNAANIRKNCKLEIDSTLYKNLF 540
OY 541 VDKNMKIPTEDVSGISLEQLRLQOEERTCKVCMDEKVSVEFIPCGHLVYCCQCAPSLR 600
DB 541 VDKNMKIPTEDVSGISLEQLRLQOEERTCKVCMDEKVSVEFIPCGHLVYCCQCAPSLR 600
OY 601 KCPICRGIIKGTVPFLS 618
DB 601 KCPICRGIIKGTVPFLS 618

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RESULT 7
AAW13555 standard; Protein: 612 AA.

AAW13555;

22-JUL-1997 (first entry)

Murine c-IAP.

IAP; Inhibitor; apoptosis; RING finger domain; restinosis;

myocardial infarction; nephritis; HIV.

Mus musculus.

MO9706182-A1.

20-FEB-1997.

06-AUG-1996; 96WO-US12860.

08-DEC-1995; 95US-0569749.

08-AUG-1995; 95US-0512946.

(TULA-) TULARIK INC.

Goeddel DV, Rothe M;

WPI; 1997-154209/14.

N-PSDB; AAT61592.

Nucleic acids encoding cellular inhibitor of apoptosis proteins
useful for apoptosis regulation in cells to reduce or increase
apoptosis and for pharmacological screening

Disclosure; Page 28-29; 35pp; English.

The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
AAT61590/T61591) comprise a series of defined structural domain
repeats and/or a RING finger domain; in particular, at least two of
a first domain repeat (AAW13547 or AAW13548), a second domain repeat
(AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
sequences derived from these human genes.
The nucleic acid is used for recombinant prodn. of human cellular
inhibitor of apoptosis protein which modulates apoptosis
regulation. The nucleic acids are useful in therapies where
increased cell-specific apoptosis is desired, e.g. in restinosis,
inflammatory disease states, myocardial infarction, glomerular
nephritis, transplant rejection and infectious diseases, e.g. HIV.
They can also be used in conditions requiring a reduction in

CC apoptosis.
XX Sequence 612 AA;

Query Match 83.2%; Score 2728; DB 18; Length 612;
Best Local Similarity 83.4%; Pred. No. 2.3e-235;
Matches 517; Conservative 45; Mismatches 48; Indels 10; Gaps 6;

```

OY 1 MKTAQORLPFGPSQONIKSIMEEDSTILSDWTNKNKQKMYDSCCELYRMSTYTFAGV 60
DB 1 MDKTVSQRLGGTLLHQKLRIMEKSTILSNMTKESEKKKFDSCCELYRMSTYTFAGV 60
OY 61 PVSESLARAGFYFYGVNDKVKFCGCCGLMDNMKLGDSPIQKRLQYPSCTQNTLSAS 120
DB 61 PVSESLARAGFYFYGVNDKVKFCGCCGLMDNMKLGDSPIQKRLQYPSCTQNTLSAS 120
OY 121 LGSTSKNTSPMRNSPAHSLSPTLEHSLSFGSYSSLSPNPLNSRAVEDISSRTPSYA 180
DB 121 LGSTSKNTSPMRNSPAHSLSPTLEHSLSFGSYSSLSPNPLNSRAVEDISSRTPSYA 180
OY 181 MSTEARFLTYHMMPLTFILSPSELARAGFYIIGPDRAVACFACGGKLSNMEPRDAMSEH 240
DB 174 MSTEARFLTYHMMPLTFILSPSELARAGFYIIGPDRAVACFACGGKLSNMEPRDAMSEH 240
OY 241 RHFPCPFLENSLETLRBSISNLSMOTHAARKMTFTWPSVPVQPEQLASAGFYVGR 300
DB 234 RHFPCPFLENSLETLRBSISNLSMOTHAARKMTFTWPSVPVQPEQLASAGFYVGR 293
OY 301 NDDVKCFCCDGLRCWESGDDPWVEHAKWFPCEFLIRKQGEFVDEIQGRYPHLEQL 360
DB 294 NDDVKCFCCDGLRCWESGDDPWVEHAKWFPCEFLIRKQGEFVDEIQGRYPHLEQL 353
OY 361 STSDTGEENADPPIIHFGPESSESDAVMMNTPVYKSALEMGFNRDLVQTVQSKILT 418
DB 354 STSDTGEENADPPIIHFGPESSESDAVMMNTPVYKSALEMGFNRDLVQTVQSKILT 412
OY 419 TTGENYKTVNDIVSALNAEDEKREERKEKQAEEMASDDLIRKNRMALFQQLCVLP 478
DB 413 TTGENYKTVNDIVSALNAEDEKREERKEKQAEEMASDDLIRKNRMALFQQLCVLP 472
OY 479 LDNLKANVINKQEHDIKQKQIPLQARELIDTILVKGNAANIRKNCKLEIDSTLYKN 538
DB 473 LDNLKANVINKQEHDIKQKQIPLQARELIDTILVKGNAANIRKNCKLEIDSTLYKN 532
OY 539 LEVDKMKKIPTEDVSGISLEQLRLQOEERTCKVCMDEKVSVEFIPCGHLVYCCQCAPS 598
DB 533 LEVDKMKKIPTEDVSGISLEQLRLQOEERTCKVCMDEKVSVEFIPCGHLVYCCQCAPS 592
OY 599 LKCPICRGIIKGTVPFLS 618
DB 593 LKCPICRGIIKGTVPFLS 612

```

RESULT 8
AAW69299 standard; Protein: 612 AA.

AAW69299;

13-NOV-1998 (first entry)

Murine HIAP-2 protein.

Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;

proliferative disease; IAP; therapy; cancer; mouse; HIAP-2 protein.

Mus sp.

MO9835693-A2.

20-AUG-1998.

13-FEB-1998; 98WO-IB00781.

XX 13-FEB-1997; 97US-0800929.
 XX (UYOT-) UNIV OTTAWA.
 PA Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
 PI Tsang B;
 XX WPI: 1998-467164/40.
 DR N-PSDB; AAV55043.
 XX
 PT Inducing apoptosis in proliferative mammalian cells with inhibitor
 PT of IAP or NAIP polypeptide - also methods for prognosis based on
 PT presence of IAP and NAIP, specifically applied to cancers involving
 PT p53 mutations
 XX
 PS Disclosure; Fig 6; 147pp; English.
 XX
 CC This sequence is the murine HIAP-2 protein, which is an inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors.
 XX
 SQ Sequence 612 AA;
 Query Match 83.1%; Score 2724; DB 15; Length 612;
 Best Local Similarity 83.2%; Pred. No. 5.2e-235;
 Matches 516; Conservative 46; Mismatches 48; Indels 10; Gaps 6;
 QY 1 MHKTSORLPFGPSYONIKSIMEDSTLLSDWTNSNOKMYDFSCELYRMSTYSPAGV 60
 DB 1 MDKTVSQRKGGTILHOKIKRIMEKSTLLSNWTKSEKMKDFSCELYRMSTYSAFPRGV 60
 QY 61 PVSESLARAGFYTGVDKVCFCGGLMDWMLKDGSPQKHKOYSPSCFIQNLVSAS 120
 DB 61 PVSESLARAGFYTGVDKVCFCGGLMDWMLKDGSPQKHKOYSPSCFIQNLVSAS 120
 QY 121 LGSTSKNTSPMRNSFAHSLPTLHSLFSGSYSLSPNPLNSRAVEDISSRTNPYSTA 180
 DB 121 LGSTSKNTSPMRNSFAHSLPTLHSLFSGSYSLSPNPLNSRAVEDISSRTNPYSTA 180
 QY 181 MSTEERARFLTYHMPFLFLSPSELARAGFYTGPDVACAGCGKLSNMPKDDAMSEH 240
 DB 174 MSTEERARFLTYHMPFLFLSPSELARAGFYTGPDVACAGCGKLSNMPKDDAMSEH 240
 QY 241 RRHFPNCPLENSLETFLSFISNLSMOTHAARMRTFMYWPSVVPVPEOLASAGFYVGR 300
 DB 241 RRHFPNCPLENSLETFLSFISNLSMOTHAARMRTFMYWPSVVPVPEOLASAGFYVGR 300
 QY 234 RRHFPNCPLENSLETFLSFISNLSMOTHAARMRTFMYWPSVVPVPEOLASAGFYVGR 293
 DB 234 RRHFPNCPLENSLETFLSFISNLSMOTHAARMRTFMYWPSVVPVPEOLASAGFYVGR 293
 QY 301 NDVYKFCFCDDGLRCWESGDDPVEHAKWPRCEFLIRMGGEVDEIOGVRPHLEQL 360
 DB 294 NDVYKFCFCDDGLRCWESGDDPVEHAKWPRCEFLIRMGGEVDEIOGVRPHLEQL 360
 QY 361 STSTGTGENADP--PIHFGESSESDAVMNTPVYKSALENGENRDLVKQTVOSKIL 418
 DB 354 STSTGTGENADP--PIHFGESSESDAVMNTPVYKSALENGENRDLVKQTVOSKIL 418
 QY 419 TTGENYKTVNDIVSALNAEDEKEREKEKAEMASDDLIRKRNMALEFQOLTCVLP 478
 DB 413 ATGENYKTVNDIVSALNAEDEKEREKEKAEMASDDLIRKRNMALEFQOLTCVLP 478
 QY 479 LDNLKANYINKQEHDIKQKTIPLQARELIDTILYKGNAAANIFKNCLKEIDSTLYKN 538

DB 473 LDNLKANYINKQEHDIKQKTIPLQARELIDTILYKGNAAANIFKNCLKEIDSTLYKN 532
 QY 539 LFVDMKMYIPTEDVSGLSLEBOLRRLOEERTCKVCMDEKYSVFPICGHLVCOECAPS 598
 DB 533 LFVEKNMYIPTEDVSGLSLEBOLRRLOEERTCKVCMDEKYSVFPICGHLVCOECAPS 592
 QY 599 LRKPCICGIIKCTVTFELS 618
 DB 593 LRKPCICGIIKCTVTFELS 612
 RESULT 9
 AAW19586
 ID AAW19586 standard; Protein; 591 AA.
 XX
 AC AAW19586;
 XX
 DT 02-SEP-1997 (first entry)
 XX
 DE Mouse apoptosis inhibitor M-HIAP-2.
 XX
 KW Apoptosis inhibitor; M-HIAP-2; HIV; AIDS; neurodegeneration;
 KW myelodysplastic syndrome; ischemia; myocardial infarction; stroke;
 KW reperfusion injury; toxin-induced liver disease; gene therapy;
 KW diagnosis.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 25..92
 FT Domain /label= BIR-1
 FT Domain 156..222
 FT Domain /label= BIR-2
 FT Domain 241..308
 FT Domain /label= BIR-3
 FT Domain 541..578
 FT Domain /label= Ring_zinc_finger
 XX
 PN W09706255-A2.
 XX
 PD 20-FEB-1997.
 XX
 PF 05-AUG-1996; 96MO-IB01022.
 XX
 PR 22-DEC-1995; 95US-0576956.
 PR 04-AUG-1995; 95US-0511485.
 XX
 PA (UYOT-) UNIV OTTAWA.
 XX
 PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
 XX
 DR WPI: 1997-154262/14.
 DR N-PSDB; AAT70841.
 XX
 PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
 PT of susceptibility to apoptotic disease
 XX
 PS Claim 30; Page 100-102; 219pp; English.
 XX
 CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
 CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
 CC are inhibitors of apoptosis (IAP) and which are characterized by
 CC the presence of a ring zinc finger domain (see also AAW19587) and at
 CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
 CC The M-HIAP amino acid sequences were deduced from isolated m-hiap
 CC cDNA clones (AAT70840-41). IAP polypeptides can be expressed in host
 CC cells (in vitro or in vivo) and used in methods for treating
 CC diseases and disorders involving apoptosis, esp. in a human
 CC diagnosed as HIV-positive or as having AIDS, a neurodegenerative
 CC disease, a myelodysplastic syndrome or an ischemic injury, selected
 CC from myocardial infarction, stroke, reperfusion injury, or a toxin-

CC induced liver disease.
XX
SQ Sequence 591 AA;

Query Match 81.0%; Score 2654; DB 18; Length 591;
Best local similarity 83.8%; Pred. No. 9.4e-229;
Matches 502; Conservative 44; Mismatches 43; Indels 10; Gaps 6;

QY 22 MEDSTILSDMTNSKOKMYDFSCELYRMSTYSTPAGVPVSESRSLARAGFYTGNDKV 81
DB 1 MEKSTILSNMTKESEKMKFDFSCELYRMSTYSTAFPGRVPVSESRSLARAGFYTGNDKV 60
QY 82 KFCGGLMDNWKLGDSPIQKHQOLYPCSCFIONLVASISLSTSKNTSPMNSFASLSLSP 141
DB 61 KFCGGLMDNWKOGDSPVEKHQOLYPCSCFIONLVASISLSTSKNTSPMNSFASLSLSP 119
QY 142 TLEHSLFSGSYSLSPNPLNSRAVEDISSRTNPYSTAMSTEARFLTYHMPLEFLSP 201
DB 120 -LER---GGHNSLNCSSPLNSRAVEDF--SSRNDPCSYAMSTEARFLTYHMPLEFLSP 173
QY 202 SELARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPLENSLETFLRSI 261
DB 174 AELARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPLENSLETFLRSI 233
QY 262 SNLSMOTHAARMFTFMYSPVPQPEQLASAGFYIYGRNDVKKCCDGLRCWESGDD 321
DB 234 SNLSMOTHAARMFTFMYSPVPQPEQLASAGFYIYGRNDVKKCCDGLRCWESGDD 293
QY 322 PWVEHAKWPRCEFLIRMGQEFVDEIQRYPHLLBOLLSTSDTTEENADP--PIIHFG 379
DB 294 PWVEHAKWPRCEFLIRMGQEFVDEIQRYPHLLBOLLSTSDTTEENADPTEYVHFG 353
QY 380 PGESSEDAVMNTPVVKSALENGFNRLVQTVQSKILTGTGENTKTVNDIVSALLNAED 439
DB 354 PGE--SSKDVYVMSFPVKALENGFSLVROTVQRLATGENTKTVNDIVSALLNAED 412
QY 440 EKREBEKEKOEEMASDLSLRKRNMALEFQOLTCLVPLDNLKANVINKEOHDIIKOK 499
DB 413 ERREBEKEROTEEMASDLSLRKRNMALEFQOLTCLVPLDNLKANVINKEOHDIIKOK 472
QY 500 TOIPLQARELIDTLIVKNAANFEKNLKEIDSTLYKNLFYDKNMKYIPREDVSGLSLE 559
DB 473 TOIPLQARELIDTLIVKNAANFEKNLKEIDSTLYKNLFYDKNMKYIPREDVSGLSLE 532
QY 560 EQLRLQEBERTCKYCMDEKVSVPFIPCGHLYVQECAPSLKPCICIGITGVTRFLS 619
DB 533 EQLRLQEBERTCKYCMDEKVSVPFIPCGHLYVQECAPSLKPCICIGITGVTRFLS 591
RESULT 10
ABG65668
ID ABG65668 standard; Protein; 591 AA.
AC ABG65668;
XX
XX 26-AUG-2002 (first entry)
XX
XX Mouse inhibitor of apoptosis, HIAP2.
XX
XX Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
XX cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
XX pancreatic cancer; embryonic development; viral pathogenesis;
XX autoimmune disorder; neurodegenerative disease; multiple sclerosis;
XX lupus erythematosus; herpes virus infection; pox virus infection;
XX adenovirus infection; proliferative disease.
OS Mus. sp.
XX
XX WO200226968-A2.
XX
XX 04-APR-2002.
XX
XX 27-SEP-2001; 2001WO-CA01379.

XX 28-SEP-2000; 2000US-0672717.
XX
XX (UYOT-) UNIV OTTAWA.
XX PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Korneiluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX
XX MPI; 2002-479562/51.
XX N-PSDB; ABK93874.
XX
XX Novel antisense inhibitor of apoptosis nucleic acid useful for
XX enhancing apoptosis in a cell, for treating cancer and other
XX proliferative diseases
XX
XX Disclosure; Fig 6; 135pp; English.

The invention relates to an inhibitor of apoptosis (IAP) antisense
nucleic acid (I) that inhibits IAP biological activity, regardless of
length of the antisense nucleic acid, the IAP proteins may be mouse
or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
composition comprising a mammalian IAP antisense molecule and a method of
enhancing apoptosis in a cell, comprising administering a negative
regulator of the IAP anti-apoptotic pathway to the cell. The IAP
antisense inhibitor is useful for enhancing apoptosis in a cell in a
mammal diagnosed with a proliferative disease. The method is useful for
treating a patient diagnosed with a proliferative disease like cancer.
The IAP antisense molecule is useful to treat, ameliorate, improve,
sustain or prevent proliferative diseases (e.g. ovarian cancer,
adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
conditions where apoptosis is involved or implicated (e.g. embryonic
development, viral pathogenesis, autoimmune disorders, neurodegenerative
diseases, multiple sclerosis, lupus erythematosus and infection by herpes
virus, pox virus and adenovirus). The present sequence is a mouse IAP
protein sequence.

XX
SQ Sequence 591 AA;

Query Match 81.0%; Score 2654; DB 23; Length 591;
Best local similarity 83.8%; Pred. No. 9.4e-229;
Matches 502; Conservative 44; Mismatches 43; Indels 10; Gaps 6;

QY 22 MEDSTILSDMTNSKOKMYDFSCELYRMSTYSTPAGVPVSESRSLARAGFYTGNDKV 81
DB 1 MEKSTILSNMTKESEKMKFDFSCELYRMSTYSTAFPGRVPVSESRSLARAGFYTGNDKV 60
QY 82 KFCGGLMDNWKLGDSPIQKHQOLYPCSCFIONLVASISLSTSKNTSPMNSFASLSLSP 141
DB 61 KFCGGLMDNWKOGDSPVEKHQOLYPCSCFIONLVASISLSTSKNTSPMNSFASLSLSP 119
QY 142 TLEHSLFSGSYSLSPNPLNSRAVEDISSRTNPYSTAMSTEARFLTYHMPLEFLSP 201
DB 120 -LER---GGHNSLNCSSPLNSRAVEDF--SSRNDPCSYAMSTEARFLTYHMPLEFLSP 173
QY 202 SELARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPLENSLETFLRSI 261
DB 174 AELARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPLENSLETFLRSI 233
QY 262 SNLSMOTHAARMFTFMYSPVPQPEQLASAGFYIYGRNDVKKCCDGLRCWESGDD 321
DB 234 SNLSMOTHAARMFTFMYSPVPQPEQLASAGFYIYGRNDVKKCCDGLRCWESGDD 293
QY 322 PWVEHAKWPRCEFLIRMGQEFVDEIQRYPHLLBOLLSTSDTTEENADP--PIIHFG 379
DB 294 PWVEHAKWPRCEFLIRMGQEFVDEIQRYPHLLBOLLSTSDTTEENADPTEYVHFG 353
QY 380 PGESSEDAVMNTPVVKSALENGFNRLVQTVQSKILTGTGENTKTVNDIVSALLNAED 439
DB 354 PGE--SSKDVYVMSFPVKALENGFSLVROTVQRLATGENTKTVNDIVSALLNAED 412
QY 440 EKREBEKEKOEEMASDLSLRKRNMALEFQOLTCLVPLDNLKANVINKEOHDIIKOK 499
DB 413 ERREBEKEROTEEMASDLSLRKRNMALEFQOLTCLVPLDNLKANVINKEOHDIIKOK 472

PI Goeddel DV, Rothe M;
 XX WPI: 1997-154209/14.
 DR N-PSDB: AAT61591.

XX Nucleic acids encoding cellular inhibitor of apoptosis proteins
 PT useful for apoptosis regulation in cells to reduce or increase
 PT apoptosis and for pharmacological screening

PS Disclosure: Page 21-23; 35pp; English.

XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
 CC AAT61590/T61591) comprise a series of defined structural domain
 CC repeats and/or a RING finger domain; in particular, at least two of
 CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
 CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
 CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
 CC sequences derived from these human genes.
 CC The nucleic acid is used for recombinant prodn. of human cellular
 CC inhibitor of apoptosis protein which modulates apoptosis
 CC regulation. The nucleic acids are useful in therapies where
 CC increased cell-specific apoptosis is desired, e.g. in restinosis;
 CC inflammatory disease states, myocardial infarction, glomerular
 CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
 CC They can also be used in conditions requiring a reduction in
 CC apoptosis.

XX Sequence 604 AA;

Query Match 71.8%; Score 2353; DB 18; Length 604;
 Best Local Similarity 72.8%; Pred. No. 9.4e-202;
 Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;

OY 20 SIMEDSTILSDWTNS-NKQKMKYDFSCCELYRMSTYSTPAGVPSERSLARAGFYTGYN 78
 DB 2 NIVENSIFLSNLMKSNANTFELKYDLSCELYRMSTYSTPAGVPSERSLARAGFYTGYN 61
 OY 79 DKVCCGCGMLDNMKLGDSPIDKHKOLYPCSCFTQNLVSA-SLGSTSKNTSP--MKNSE 135
 DB 62 DKVCCGCGMLDNMKLGDSPIDKHKOLYPCSCFTQNLVSA-SLGSTSKNTSP--MKNSE 135
 OY 136 AHSLSPTLEHSSLSFGSYSSLSPLNRAVEDISSKRNPFYAMSTEARFLTYHWP 195
 DB 121 THSLPGETENGCFRGSYSNSPNSVNSRANQDSALMRSSVHCAMNENARLLFTQWP 180
 OY 196 LTFLSPELARAAGFYIGPDRAVACGKLSNWEPRKDANSEHRRHPCPFLNSL- 254
 DB 181 LTFLSPTDLAKAGFYIIGPDRAVACGKLSNWEPRKDANSEHRRHPCPFLNSL- 240
 OY 255 ETLRFISISNLSMOTHAARMFTWPSYVOPQOLASAGFYVGRNDVKCCDGLR 314
 DB 241 DTSRYVSNLSMOTHAARMFTWPSYVOPQOLASAGFYVGRNDVKCCDGLR 300
 OY 315 CWESGDDPWVHAHAKFPRCEFLIRKKGFEVDEIOGRPHLLSOLLSTDTGEANDP 374
 DB 301 CWESGDDPWVHAHAKFPRCEFLIRKKGFEVDEIOGRPHLLSOLLSTDTGEANDP 360
 OY 375 IIFHGEGSSSEDVAMNTPVVKSALMFGFNRIYKQVOSK:LTFTGENYKTVNDYSAL 434
 DB 361 IIFHGEGSSSEDVAMNTPVVKSALMFGFNRIYKQVOSK:LTFTGENYKTVNDYSAL 420
 OY 435 LNAEDEKREERKEKQAEASDLSLRKRNMAFOQLTCLF:ILDNLKANYINKOEHD 494
 DB 421 LNAEDEKREERKEKQAEASDLSLRKRNMAFOQLTCLF:ILDNLKANYINKOEHD 480
 OY 495 IIKQKQIPLQARELIDTILVKGNAANIEKNCLEIDSTLYKNLFVKNMKYIPFEDVS 554
 DB 481 VIKQKQIPLQARELIDTILVKGNAANIEKNCLEIDSTLYKNLFVKNMKYIPFEDVS 540
 OY 555 GLSLEBQLRLQEBERTCKVMDKEYSVFIIPCGHLVVOECAPSLRKPCIGKIITVTR 614
 DB 541 DLPEBQLRLQEBERTCKVMDKEYSVFIIPCGHLVVOECAPSLRKPCIGKIITVTR 600

OY 615 TFLS 618
 DB 601 TFLS 604

RESULT 13

AAV52703 standard; Protein: 604 AA.

AAV52703;

26-JAN-2000 (first entry)

Human cellular inhibitor of apoptosis-2 protein.

Identification; genetic target; gene modulation; human;
 antisense oligonucleotide; phosphorothioate; target validation;
 nucleotide sequence-based technology; antisense drug discovery.

Homo sapiens.

MO9953101-A1.

21-OCT-1999.

13-APR-1999; 99WO-US08268.

13-APR-1998; 98US-0081483.

28-APR-1998; 98US-0067638.

(ISIS-) ISIS PHARM INC.

Cowser LM, Baker BF, McNeil J, Freiler SM, Sasnor HM, Brooks DG;
 Ohasi C, Wyatt JR, Borchers AH, Vickers TA;

WPI: 1999-620446/53.

N-PSDB: AAZ41005.

Identifying compounds which modulate expression of nucleic acids, used
 to provide compounds having defined physical, chemical or bioactive
 properties, e.g. antisense activity

Example 20; Page 197-202; 264pp; English.

A method has been developed of defining a set of compounds that modulate
 the expression of a target nucleic acid (tNA) sequence via binding of
 the compounds with the tNA sequence. The method comprises generating a
 library of virtual compounds in silico according to defined criteria,
 and evaluating in silico the binding of the virtual compounds with the
 tNA according to defined criteria. Also described are: (1) a method of
 defining a set of oligonucleotides (ONS) that modulate the expression of
 a tNA sequence via binding of the ONS with the tNA sequence comprising
 generating a library of virtual compounds in silico according to defined
 criteria, and evaluating in silico the binding of the virtual ONS with
 the tNA according to defined criteria; and (2) a method of defining a
 set of compounds that modulate the expression of a tNA sequence via
 binding of the compounds with the tNA. The methods can be used for the
 generation and identification of synthetic compounds having defined
 physical, chemical or bioactive properties. Information gathered from
 assays of such compounds is used to identify nucleic acid sequences that
 are tractable to a variety of nucleotide sequence-based technologies,
 e.g. antisense drug discovery and target validation. AAZ40852 to
 AAZ41220, and AAV52701 to AAV52706, represent sequences used in the
 exemplification of the present invention.

Sequence 604 AA;

Query Match 71.8%; Score 2353; DB 20; Length 604;
 Best Local Similarity 72.8%; Pred. No. 9.4e-202;
 Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;

OY 20 SIMEDSTILSDWTNS-NKQKMKYDFSCCELYRMSTYSTPAGVPSERSLARAGFYTGYN 78
 DB 2 NIVENSIFLSNLMKSNANTFELKYDLSCELYRMSTYSTPAGVPSERSLARAGFYTGYN 61

```

Db 2 NIVENSIFLSNLMKSAANTFELKYLDELSCELYRMSTYSTFVAGVPSERSLARAGFYTGYN 61
QY 79 DKVKECCGMLDNMKLGDSPIQKHQKQLYPSCSEFIQNIYSA-SLGSTSKNTSP--MRNSF 135
DB 62 DKVKECCGMLDNMKRGDSPTKHKKLYPSCRFVQSLNVNLEATSQPTFPSSVTNS- 120
QY 136 AHSLEPTEHSLFSGSYSSLPNPLNSRAVEDISSSTPNPYASMTSEARFLTYHMP 195
DB 121 THSLPTEHSGYFSGSYSSPNPNNSRANODESALMRSSYCAMNENARLLTFQTP 180
QY 196 LTFLEPSELARAGFYIIGPDRAVACFACGKLSMWEPRKDDAMSEHRRFPNCPLESL- 254
DB 181 LTFLEPTEHSLFSGSYSSLPNPLNSRAVEDISSSTPNPYASMTSEARFLTYHMP 240
QY 255 ETLRSISNLSMOTHAARMFTMYWPSVYVQPEQLASAGFYVGRNDVCKFCDDGGLR 314
DB 241 DTSRYVSNLSMOTHAARMFTMYWPSVYVQPEQLASAGFYVGRNDVCKFCDDGGLR 300
QY 315 CWESGDDPWYEHAKWPPRCFELIRKKGQEFVDEIQRYPHLEQLLSTSDTTEENADP 374
DB 301 CWESGDDPWYEHAKWPPRCFELIRKKGQEFVDEIQRYPHLEQLLSTSDTTEENADP 360
QY 375 IIFGPGESSSEDVAMNTPVVKSALEMGNRDLVKQVQSKILLTGENTKTYNDIYSAL 434
DB 361 IIFGPGEDHSEDAIMNTPVINAEMGFSSLVKQVQSKILLTGENTKTYNDIYSAL 420
QY 435 LNAEDKREERERATEEESKNDLLIRKRMALFOHLTCVIRPILDSLTAGIINEQEH 480
DB 421 LNAEDKREERERATEEESKNDLLIRKRMALFOHLTCVIRPILDSLTAGIINEQEH 480
QY 495 IIKQKQIPIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLFYDKMKYIPTEDVS 554
DB 481 VIKQKQIPIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLFYDKMKYIPTEDVS 540
QY 555 GLSLEQLRLQEFRTCKYCMDEKESVVFIPCGHLVVOECAPSLRKPCIRGIIKGTVR 614
DB 541 DLPEBQLRLQEFRTCKYCMDEKESVVFIPCGHLVVOECAPSLRKPCIRGIIKGTVR 600
QY 615 TFLS 618
DB 601 TFLS 604

```

RESULT 14
AAV33997
ID AAV33997 standard; Protein; 604 AA.

AC AAV33997;
XX
DT 26-NOV-1999 (first entry)
XX
DE Human cellular inhibitor of apoptosis-2 sequence.
XX
KM Cellular inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;
XX c-IAP-2; prophylaxis; infection; inflammation; tumor formation.
XX
OS Homo sapiens.
XX
PN US958771-A.
XX
PD 28-SEP-1999.
XX
PF 03-DEC-1998; 98US-0205144.
XX
PR 03-DEC-1998; 98US-0205144.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowser LM, Ackermann EJ;
XX
DR WPI; 1999-561046/47.
XX
DR N-PSDB; AA22096.
XX

```

PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2
PI useful for e.g. diagnostics, therapeutics, and as research reagents -
XX
XX Example 13; Columns 45-50; 33pp; English.
XX
CC The invention provides antisense compounds of 8-30 nucleotides that
CC inhibit the expression of human Cellular Inhibitor of Apoptosis-2
CC (c-IAP-2). The antisense compounds may be used for diagnostics,
CC therapeutics (for modulating the expression of c-IAP-2), prophylaxis
CC (e.g. to prevent or delay infection, inflammation, or tumor formation),
CC as research reagents (e.g. to distinguish between members of a biological
CC pathway) and in kits. The present sequence represents the human cellular
CC inhibitor of apoptosis-2.
XX
SQ Sequence 604 AA;

```

Query Match 71.8%; Score 2353; DB 20; Length 604;
Best Local Similarity 72.8%; Pred. No. 9.4e-202;
Matches 440; Conservative 71; Mismatches 87; Indels 6; Gaps 5;

```

QY 20 SIMEDSTLSDWTNS-NKQKMYDFSCELYRMSTYSTFPAGVPSERSLARAGFYTGYN 78
DB 2 NIVENSIFLSNLMKSAANTFELKYLDELSCELYRMSTYSTFPAGVPSERSLARAGFYTGYN 61
QY 79 DKVKECCGMLDNMKLGDSPIQKHQKQLYPSCSEFIQNIYSA-SLGSTSKNTSP--MRNSF 135
DB 62 DKVKECCGMLDNMKRGDSPTKHKKLYPSCRFVQSLNVNLEATSQPTFPSSVTNS- 120
QY 136 AHSLEPTEHSLFSGSYSSLPNPLNSRAVEDISSSTPNPYASMTSEARFLTYHMP 195
DB 121 THSLPTEHSGYFSGSYSSPNPNNSRANODESALMRSSYCAMNENARLLTFQTP 180
QY 196 LTFLEPSELARAGFYIIGPDRAVACFACGKLSMWEPRKDDAMSEHRRFPNCPLESL- 254
DB 181 LTFLEPTEHSLFSGSYSSLPNPLNSRAVEDISSSTPNPYASMTSEARFLTYHMP 240
QY 255 ETLRSISNLSMOTHAARMFTMYWPSVYVQPEQLASAGFYVGRNDVCKFCDDGGLR 314
DB 241 DTSRYVSNLSMOTHAARMFTMYWPSVYVQPEQLASAGFYVGRNDVCKFCDDGGLR 300
QY 315 CWESGDDPWYEHAKWPPRCFELIRKKGQEFVDEIQRYPHLEQLLSTSDTTEENADP 374
DB 301 CWESGDDPWYEHAKWPPRCFELIRKKGQEFVDEIQRYPHLEQLLSTSDTTEENADP 360
QY 375 IIFGPGESSSEDVAMNTPVVKSALEMGNRDLVKQVQSKILLTGENTKTYNDIYSAL 434
DB 361 IIFGPGEDHSEDAIMNTPVINAEMGFSSLVKQVQSKILLTGENTKTYNDIYSAL 420
QY 435 LNAEDKREERERATEEESKNDLLIRKRMALFOHLTCVIRPILDSLTAGIINEQEH 480
DB 421 LNAEDKREERERATEEESKNDLLIRKRMALFOHLTCVIRPILDSLTAGIINEQEH 480
QY 495 IIKQKQIPIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLFYDKMKYIPTEDVS 554
DB 481 VIKQKQIPIQARELIDTILVKGNAANIFKNCLEIDSTLYKNLFYDKMKYIPTEDVS 540
QY 555 GLSLEQLRLQEFRTCKYCMDEKESVVFIPCGHLVVOECAPSLRKPCIRGIIKGTVR 614
DB 541 DLPEBQLRLQEFRTCKYCMDEKESVVFIPCGHLVVOECAPSLRKPCIRGIIKGTVR 600
QY 615 TFLS 618
DB 601 TFLS 604

```

RESULT 15
AAW19582
ID AAW19582 standard; Protein; 604 AA.

AC AAW19582;
XX
DT 02-SEP-1997 (first entry)
XX

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:58:42 ; Search time 67.6382 Seconds

(without alignments)
878.365 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277
Sequence: 1 MHKTASQRLFPSPSYONIKS.....LRKCPICRGIIKGVRTFLS 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3247	99.1	618	2	S68450	apoptosis inhibitor
2	2332	71.2	604	2	S68449	apoptosis inhibitor
3	1532	46.8	358	2	JC5964	apoptosis inhibitor
4	908	27.7	497	2	S69544	apoptosis inhibitor
5	737	22.5	497	2	S69545	apoptosis inhibitor
6	723.5	22.1	496	2	S68452	apoptosis inhibitor
7	513	15.7	268	2	T10304	inhibitor of apoptosis
8	513	15.7	268	2	A53989	neutrophil apoptosis
9	468	14.3	1447	2	T42628	neuronal apoptosis
10	463	14.1	1232	2	A55478	inhibitor of apoptosis
11	461	14.1	275	2	A45679	inhibitor of apoptosis
12	460.5	14.1	298	2	JC7568	inhibitor of apoptosis
13	240	7.3	292	2	T41772	inhibitor of apoptosis
14	237.5	7.2	997	2	T43523	inhibitor of apoptosis
15	235.5	7.2	286	2	D36828	inhibitor of apoptosis
16	223.5	6.8	275	2	T10310	inhibitor of apoptosis
17	194	5.9	4845	2	T31067	BIR repeat containing
18	186.5	5.7	316	2	T32659	hypothetical protein
19	181.5	5.5	711	2	C84767	hypothetical protein
20	175.5	5.4	208	2	T03183	probable apoptosis
21	169	5.2	150	2	T28409	ORF MSV248 probable
22	165	5.0	943	2	S68824	ring protein, cytochrome
23	161	4.9	155	2	T30489	apoptosis inhibitor
24	156	4.8	823	2	D86165	protein F15K9.3 [15K9.3]
25	152	4.6	234	2	T30427	probable apoptosis
26	152	4.6	304	2	T04751	hypothetical protein
27	146	4.5	870	2	G86450	F5D14.31 protein
28	144	4.4	249	2	H72858	apoptosis inhibitor
29	142	4.3	249	2	T41814	IAP2 orf71 - Bombyx

30	140.5	4.3	785	2	T00474	hypothetical prote
31	138	4.2	372	2	C96631	hypothetical prote
32	137.5	4.2	236	2	T10343	inhibitor of apopt
33	137	4.2	614	2	S42526	finger protein unk
34	136.5	4.2	864	2	T01393	apoptosis inhibitor
35	131.5	4.0	899	2	D96594	unknown protein, 7
36	131	4.0	308	2	T37474	apoptosis inhibitor
37	130	4.0	115	2	B96664	probable RING: zinc
38	129.5	4.0	329	2	T28403	ORF MSV242 probabl
39	128	3.9	347	2	T01044	hypothetical prote
40	128	3.9	1639	2	T50119	probable sensory t
41	126	3.8	145	2	S77736	probable zinc fing
42	124.5	3.8	383	2	F96582	hypothetical prote
43	124	3.8	433	2	JC7678	RING finger protei
44	122	3.7	2364	2	T40884	cytoxin L - Clos
45	121.5	3.7	708	2	T00064	hypothetical prote

ALIGNMENTS

RESULT 1

S68450

apoptosis inhibitor hiap-2 - human

C:Species: Homo sapiens (man)

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #ext_change 21-Jul-2000

C:Accession: S68450

R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chertton-Horvat, G.; Faraha

Nature 379, 349-353, 1996

A>Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of

A:Reference number: A58182; MWID:96149249; PMID:8552191

A:Accession: S68450

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-618 <LIS>

A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; FID:g1184318

C:Function:

A:Description: apoptotic suppressor

C:Superfamily: RING finger homology

C:Keywords: apoptosis; zinc finger

F:567-611/Domain: RING finger homology <RNG>

Query Match	Best Local Similarity	Score	Pred. No.	DB 2;	Length	615;
Matches 614;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;		
QY	1	MHKTASQRLFPSPSYONIKS	IMEDSTIISDWTNSNKKQKKYDFSCDLYRMSTYSPAGV	60		
DB	1	MHKTASQRLFPSPSYONIKS	IMEDSTIISDWTNSNKKQKKYDFSCDLYRMSTYSPAGV	60		
QY	61	PVSERSLAGFYTYGVNDKVKFCGGLMDNKLGDSPIDKHKOLYPCSFIONIVSAS	120			
DB	61	PVSERSLAGFYTYGVNDKVKFCGGLMDNKLGDSPIDKHKOLYPCSFIONIVSAS	120			
QY	121	LGSTKNTSPMRNSFAHSLSPTEHSSLSFGSSYSSLSNPPLNSRAVEDISSRTNPXYA	180			
DB	121	LGSTKNTSPMRNSFAHSLSPTEHSSLSFGSSYSSLSNPPLNSRAVEDISSRTNPXYA	180			
QY	181	MSTEARFLTYHMDLTLSPSELARAGFYIIGPGDRVACFACGKLSNWEKPDAMSEH	240			
DB	181	MSTEARFLTYHMDLTLSPSELARAGFYIIGPGDRVACFACGKLSNWEKPDAMSEH	240			
QY	241	RRHFPNCPFLNLSLETLREISINLSMOTHAARMFTFWPSSVVPVQEQLASAGFYVGR	300			
DB	241	RRHFPNCPFLNLSLETLREISINLSMOTHAARMFTFWPSSVVPVQEQLASAGFYVGR	300			
QY	301	NDDVCFCCDGLRCWESGDDPWVEHAKWPRCEFLIRMKGOEFVDEIOGRPHLEQL	360			
DB	301	NDDVCFCCDGLRCWESGDDPWVEHAKWPRCEFLIRMKGOEFVDEIOGRPHLEQL	360			
QY	361	STSDTTGEENADPPIIHFGPGESESDAVMNTPVVKSALENGFNRLVVKQVLSKILTT	420			
DB	361	STSDTTGEENADPPIIHFGPGESESDAVMNTPVVKSALENGFNRLVVKQVLSKILTT	420			

C:Species: Homo sapiens (man)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S69544; S68451
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C.
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69544
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: EMBL:U32974; NID:g1016687; PION:AAC50518.1; PID:g1016688
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68451
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>
A:Cross-references: EMBL:U45880; NID:g1184319; PION:AAC50373.1; PID:g1184320
C:Genetics:
A:Gene: 11p
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

Query Match 27.7%; Score 908; DB 2; Length 497;
Best Local Similarity 33.8%; Pred. No. 4.8e-55;
Matches 205; Conservative 88; Mismatches 104; Indels 150; Gaps 14;

OY 35 NKQKMYDFSCSELYRSTYTFPAGVPVSESLARAGFYTYGVNDKVKCFCCGLMDNWK 94
DB 18 NKEE---EFVEEFNRLKTFANFPSSGSPVASSTLARAGFLYTGEDTVRCFSCHAAYDRMO 74
OY 95 LGDSPLOKHQKOLYPCSCFIONLVASLSTSKNTSPMRNSF-AHSLPTLEHSSLFSGSY 153
DB 75 YGDSAVGRHRYKVPNCRFINGFYLENSATQSTNGIQNGQYKENVYLGSRDHFALDRPS 133
OY 154 SLSLPNPLNSRAVEDISSRTNPSYAMSTEARFLTYHMP-LTFLSPSELARAGFYI 212
DB 134 ETHADYLLRTGOVVDISDT-ITPRNPAMYSEARLKSFQNPDYAHLTPRELASAGLYT 192
OY 213 GPDRVACFACGCKLSNMEPKDDAMSEHRRHFPNCPFL-----EN 252
DB 193 GIGDOYQCFCCGCKLKNMEPCDRAWSEHRRHFPNCFVLGRILNIRSESDAVSSDRNFPN 252
OY 253 SLETLRFISLSMOTHAARMRTFMYWSPVPOEQLASAGFYVGRNDVKCFCCDGG 312
DB 253 STNLPF---NPSMADYEARIETFTGTWYS--VNKEQLARAGFYALGEDVKVCFHCGGG 306
OY 313 LRCWESGDDPWEVHAHAKWFPCEFLIRMGQEFVDEIOGRYPHLEQ-LISTSDTTGEENA 371
DB 307 LTDWKSSEDPRQOAHKWPCKCYLLEQKGOEYINNI--HLTSLSECLVTRTEKT----- 359
OY 372 DPEIHFGPSSSEDVAVMNTPVYKSALEMGNRDVYKOTVOSKILTTGENKTVNDIV 431
DB 360 -----PSLTRLRIDDTIFQNPVQEAIRMGFSFKDIKIMEKIQISGSNYKSLLEVLY 411
OY 432 SALLNADEKREERKEQAEMASDLSLRKNMALFOQLTVLPITDNLKANVINKO 491
DB 412 ADLVNAQKDSMPDE----- 425
OY 492 EHDIIKOKTQIPLQARELIDTILVKGMAANIFKNCLKEIDSTLYKNLFVDKNMKYIPT 551
DB 426 -----SSQTSLO-----KEI----- 435
OY 552 DVSGLSEEDRLQERTCKVKMDKEVSVFPCGHLYVCOECAPSLRKPCIRGIITG 611
DB 436 -----STEEQLRLQEBELCKICKMDRNIAIVFPCGHLYVTCQCAEAAYDCPACVYITTF 490

OY 612 TVRTFLS 618
DB 491 KQKIFMS 497

RESULT 5
S69545
apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69545
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan,
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69545
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: EMBL:U32373; NID:g1019116; PIDN:AAC47155.1; PID:g1019117
C:Genetics:
A:Gene: 11p
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
F:446-490/Domain: RING finger homology <RRN>

Query Match 22.5%; Score 737; DB 2; Length 497;
Best Local Similarity 30.6%; Pred. No. 3.2e-43;
Matches 180; Conservative 82; Mismatches 212; Indels 114; Gaps 15;

OY 46 ELYRMSTYTFPAGVPVSESLARAGFYTYGVNDKVKCFCCGLMDNWKLGDSPIQKHQ 105
DB 9 ESVRLTFGEFGLPNAPVSAEDLVANGFATGNMLEAFCHVRIDREYEQVAAAGHR 68
OY 106 LYPSCFIONLVASLSTSKNTSPMRNSFAHSLPTLEHSSLFSGSYSSLSLPNLSRA 165
DB 69 SSPICMV--LAPNCGANVDR-----SOESDNEGNS-- 97
OY 166 VEDISSRTNPSYAMSTEARFLTYHMP-LTFLSPSELARAGFYVGRNDVKVCEACGG 225
DB 98 VYDSEPCSCP---DLLENRLTYFKDMPNPTTPQALAKAGFYVGRNDVKVCEACGG 154
OY 226 KLSNMEPKDDAMSEHRRHFPNCPFL-----NSLETLRFISLSMOTH---AA 271
DB 155 VIAKWEKNDNAFEHRRHFPNCPQPRVOMGPLIEATGKNLDELGIQPTLPLPKYACVDA 214
OY 272 RMRTFMYWSPVPOE-QQLASAGFYVGRNDVKCFCCDGGGLRCWESGDDPWEVHAHAKW 330
DB 215 RLRTFTDWPIS-NIQPASALAQAGLYYQKIGDQYRCFHCNIGRSWQKEDDEPFEHAKWS 273
OY 331 PRCEFLIRMGQEFVDEIOGRYPHLEQLISTSDTTGENADPPIHFGPSSSEDVAVM 390
DB 274 PKQFVLLAGPSYSEVLA-----TTANASSPAT--APATLQADAVLM 317
OY 391 MNPVYKSALEMGNRDVYKOTVOSKILTTGENKTVNDIVSALLNADEKREERKEQA 450
DB 318 DEAP-AKALALGIDGGVANAIOKLLSSGCAFTDELHIDF----- 362
OY 451 EEMASDLSLRKNMALFOQLTVLPITDNLKANVINKQEHDIINOKTQIPLQARELI 510
DB 363 DAGAGADWRCASREPSAPF-----IEPCQATTSKA-----ASVPIPVADSI 403
OY 511 DTILVKGMAANIFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSLEEDRLQERT 570
DB 404 PAKPOAAEAVANISK-----ITDELQKMSVATPAGNLSLEENRQKADARL 449
OY 571 KVCMDKEVSVFPCGHLYVCOECAPSLRKPCIRGIITGTVRTFLS 618
DB 450 KVCVLEDEEVGVFLPCGHILATCNCAPSVANCPMRADIKGFVRTFLS 497

RESULT 6
S68452
apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)

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C:Species: Drosophila melanogaster
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Nov-2000
C:Accession: S68452; S78528
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahant,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; NUID:96149249; PMID:1552191
A:Accession: S68452
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-496 <LIS>
A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
Submitted to the EMBL Data Library, January 1996
A:Reference number: S78528
A:Accession: S78528
A:Molecule type: mRNA
A:Residues: 1-36, 'AT', 37, 'K', 39, 'L', 41-44, 'H', 46-48, 'Q', 60-612, 'A', 414-427, 'A', 429-496 <
C:Genetics:
A:Cross-references: FlyBase:FBgn0015247
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homolog
C:Keywords: apoptosis; zinc finger
F:445-489/Domain: RING finger homolog <RNG>

Query Match 22.1%; Score 723.5; DB 2; Length 496;
Best Local Similarity 30.5%; Pred. No. 2,8e-43;
Matches 180; Conservative 90; Mismatches 201; Indels 119; Gaps 18;

OY 46 ELYRMSTYSTEPAQVPSERSLARAGFYTYGVNDKVKCFCCGLMDNMKLGDSPTQKHQ 105
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 9 ESVRLATFGEPLNAPVASADLVANGFEGTWM--EACDFCHVRIIDRWEYGDVAERHRR 66
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 106 LYPSCSEIOMVSAISLSTSKNTSMRNSFAHSLSPLEHSSLSFGSVSSLPNPLNSRA 165
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 67 SSPICMV--LAPNHCNVPR-----SQESDNEGNS-- 95
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 166 VEDISSRTNYSYAMSTEARFLTHMPLTFLSPSELRARAGYYITGPDRAVACFACGG 225
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 96 VVDSPESSCSCP--DLLLEANRLVTFKDWPNPNITPQALAKAGFYLLNLDHVKVCWONG 152
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 226 KLSNWEPKDAMSEHRHFPNCPLE-----NSLETLPESISNLSMOTH---AA 271
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 153 VIATWEKNDNAFEEHRRFFPQCPRQMGPLIEFATGKNIDELGIQPTLLPLRKYACVDA 212
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 272 RMRTFMYWPSVVPQ--EQLASAGFYVGRNDVYKFCFCCDGLRCWESGDDPWVEHAKWF 330
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 213 RLRTFTDWPIS--NIDPASALAQAGLYQKTGDQVYKCFHCNIGLSWQKEDEPVEHAKWS 271
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 331 PRCEFLIRMGOEFVEIDIGRYPHLEQLLSTSDTGTGEENADPPIIHGPGESSESDAVM 390
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 272 PKCOEVLAKGPAYVSEV-----LAT--TAANASSQIPAT--APAPTLQADVLM 315
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 391 MNTPVVKSALFMGFNDLVQTVQSKILTTGENYKTVNDIVSALLNAEDEKREEKEKOA 450
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 316 DEAP-AKEALTLGIDGGVVRNAIQKLLSSGCASTLDELHLDFFDDAGAGALEVREPP 374
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 451 EEMASDLSLRKRNALFQOLTCLVLPILDNLKANVINKQEHDIKQTOIPL--QARE 508
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 375 EPSA-----PTEPCQATTSKAASVIPVADS-----IAKQAAE 410
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 509 LIDTILVKGNAANATFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSG:SLSEOLRLDOE 568
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 411 -----AVSNISK-----ITDEIQKMSVSTJNGNISLEENRQLKDA 446
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
OY 569 RTCKVCMDEKESVVFPCGHLVWQECAPSLRKCPICRGIIKGVRTFLS 618
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 447 RLCKVCLDEEYGVFLPCGHLATCNQCAPSVANCPMCRADIKGVRTFLS 496
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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T10304
inhibitor of apoptosis protein 3 - *Orygia pseudotsugata* nuclear polyhedrosis virus
C.Species: *Orygia pseudotsugata* nuclear polyhedrosis virus, OpMPV
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C.Accession: T10304
R.Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohmann, G.F.
Virology 229, 361-399, 1997
A.Title: The sequence of the *Orygia pseudotsugata* multinucleocapsid nuclear polyhedro
A.Reference number: Z17011; MUID:97271300; PMID:9126251
A.Accession: T10304
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-268 <AHR>
A.Cross-references: EMBL:U75930; NID:g2834903; PIDN:AAC59034.1; PID:g1911281
C.Superfamily: Viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

[illegible]

QY 256 TLRSIS-----NLISMT-----HAAMRTFMWPSVPVQ 286
 Db 236 ITQYISQKGFVDITGEHFNWNSVORLPMASAYCNDISIFAYEELRLDSKDWPRBSAVG 295
 QY 287 PEOLASGFYVGRNDVYKFCDCDGLRCWESGDDPWVZHAKEPFRCEFIIRMGQ-EFV 345
 Db 296 VALAKAGLEFYTGIDKIDYQFCSCGGCLEKQWEGDDPLD)HTRCFPCPLQNMKSSAEVY 355
 QY 346 DEIOGRPHLLLEQLSTSDTGTGEN--ADPPIHFGPGNS--SEDAVMNTPV----- 395
 Db 356 PDLOS-R-GELECELETSESNEEDSIAGPIPEMAQGHQWFOEAKNLNEQLRAYTSA 414
 QY 396 -----VKSAL-----MGFNRLVYKQVOSKI-----LTTGENTKYVNDIVSALLNAED 439
 Db 415 SFRHMSLIDISDLATDHLGLGDLSTASKHISKPVQEPVLPPEVGNLNSVWCVGEAGS 474
 QY 440 EKREKEKQAEEMASDLSLRKNRMALFOQLTCVLP-----ILDNLK----- 484
 Db 475 GKTYLTK-KIAFLMASGCCPLNRFOLVFTYLSSTRPDEGLASTICDQLEKEGSVTEM 533
 QY 485 --ANVINKOEHDII-----KQKTQIPLOARELID-----TLVKGNAAANI--FK 525
 Db 534 CMRNIIQOLKNQVLELLDDYKEICSIPOVIGKLIQRNHL;RTCLLIAYRTNRADIRRL 593
 QY 526 NCLKEIDSTLYKN 538
 Db 594 ETILEIQAFPEVN 606

RESULT 11

A45679
 Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CPGV
 C:Species: Cydia pomonella granulosis virus CPGV
 C:Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
 C:Accession: A45679
 R: Crook, N.E.; Ciem, R.J.; Miller, L.K.
 J. Virol. 67, 2168-2174, 1993
 A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
 A:Reference number: A45679; MUID:93188168; PMID:8445726
 A:Accession: A45679
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <CRO>
 A:Cross-references: GB:105494; NID:q289583; PIDN:AAA43835.1; PID:q289584
 A>Note: Sequence extracted from NCBI backbone (NCBI:127014, NCBI:P:127015)
 C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 14.1%; Score 461; DB 2; Length 275;
 Best Local Similarity 22.6%; Pred. No. 1.7e-24;
 Matches 103; Conservative 62; Mismatches 84; Indels 206; Gaps 9;

QY 184 EBARFLTYHMPPLTFLSPSELARAGFYIGPDRVACFAGGKLSNWEPRKDDAMSEHRRH 243
 Db 7 EBYRLNTEKWPVSELPETMAKNGFYLLGSDYVCAFCRVEIMRWKEGEDPADHKKW 66
 QY 244 FPNCPFL-----NSLETLRISINLSMOT-----AARMFTMTWPPSSVP 284
 Db 67 APCPFEVIGIDVCGSIYTN-NIQNT--THDTIIGPAHPKYAHBAARVASFHMPRCK 123
 QY 285 VOPEOLASGFYVGRNDVYKFCDCDGLRCWESGDDPWVZHAKEPFRCEFIIRMGQEF 344
 Db 124 QREPMADAGFYTGIDNTKFCYCDGLKDWEPEDVPMQOHVRFDRCAVYOLVKGRTY 183
 QY 345 VDEIGRPHLLLEQLSTSDTGTGENADPPIHFGPGNS--SEDAVMNTPVVKSALENG 403
 Db 184 VQKY-----ITEACVL-----PGENTTVSTAPVSEPIPEKI--- 216
 QY 404 FNRDLVKQTVOSKILTTGENTKYVNDIVSALLNAEDEKREBEKQAEEMASDLSLRK 463
 Db 217 -----EKEPVE----- 223
 QY 464 NRMAFLQOLTCVPIIDNLKANVINKOEHDIIKQKTQIPLOARELIDTLVKGNAAANI 523

Db 224 ----- 223
 QY 524 FKNCLEIDSTLYKNLFVDKMKYIPTEDVSGLSLEQLRLQERTCKVCMDEKVSVE 583
 Db 224 -----DSKLCIKCYECCYCF 240
 QY 584 IPCGHLVQCECAPSLRCPICRGIIKGTVRTFLS 618
 Db 241 VPCGHVACAKCALSDVKPCMKCRKIYTSVLKYFVS 275

RESULT 12

JC7568
 kidney inhibitor of apoptosis protein - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
 C:Accession: JC7568
 R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
 Biochem. Biophys. Res. Commun. 279, 820-831, 2000
 A:Title: KIAIP, a novel member of the inhibitor of apoptosis protein family.
 A:Reference number: JC7568; MUID: 21092523; PMID:11162435
 A:Contents: Fetal kidney
 A:Accession: JC7568
 A:Molecule type: mRNA
 A:Residues: 1-298 <LIN>
 C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, i

Query Match 14.1%; Score 460.5; DB 2; Length 298;
 Best Local Similarity 28.8%; Pred. No. 2.1e-24;
 Matches 126; Conservative 36; Mismatches 105; Indels 171; Gaps 13;

QY 212 ICGDRVACFAGGKLSNWEPRKDDAMSEHRRHP-----NC----- 247
 Db 1 MGRPKSAKCLHNGPQPSHMAAGDPQF--RCGPRSLGSPVLGIDTCRAMDHYDQIILQ 58
 QY 248 --PFLNSLE-----TLRFSISNLSMOTHAARMRTFMWPSVPVOPEOLASGFYVGR 300
 Db 59 LRPLTEEEEEEGAGATLSRGAFFPGSGEELRLASFYDWTAEVPELLAAGFFHGH 118
 QY 301 NDDVYKFCDCDGLRCWESGDDPWVZHAKEPFRCEFIIRMGQEFVDEIOGRPHLLLEQL 360
 Db 119 QDKVRCFFCYGGLQSWKRGDPTWTEHAKWPPSCQFLRLSKGRDVFVHSVQETH---SOLL 174
 QY 361 STSDTGTGENADPPIHFGPGSSSDAYMNTPVVKSALENGFRDLVKQTVOSKILTT 420
 Db 175 GSWD-----PWE-EPEDA---APVAPSVPASGYPE-----LPT 203
 QY 421 GENYKYVNDIVSALLNAEDEKREBEKQAEEMASDLSLRKNMALFOQLTCVLPILD 480
 Db 204 -----PRREVSESAQEPGVS----- 220
 QY 481 NLKANVINKOEHDIIKQKTQIPLOARELIDTLIVKGNAAANIFKNCLKEIDSTLYKNLF 540
 Db 221 -----PAEQR----- 226
 QY 541 VDKNMKIPTEDVSGLSLEQLRLQOERTCKVCMDEKVSVFIPCGHLVQCECAPSLR 600
 Db 227 -----AMWVLEPPGARVDAQDLRLQOERTCKVCLDRAVSIIVPCGHL--VCAECAPGLQ 280
 QY 601 KCPICRGIIKGTVRTFLS 618
 Db 281 LCPICRAVRSRVRTFLS 298

RESULT 13

T41772
 IAP1orf27 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C:Species: Bombyx mori nuclear polyhedrosis virus, BMSNPV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000
C:Accession: T41772
R:Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: 222020; MID:99281911; PMID:10355780
A:Accession: T41772
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-292 <RAM>
A:Cross-references: EMBL:L33180; NID:g3745835; PIDN:AAC63701.1; PID:g3745854
A:Experimental source: isolate T3
C:Genetics:
A:Note: 1ap1
C:Superfamily: viral apoptosis inhibitor IAP; RIM: finger homology

Query Match 7.3%; Score 240; DB 2; Length 292;
Best Local Similarity 18.0%; Pred. No. 3.7e-09;
Matches 78; Conservative 41; Mismatches 96; Indels 218; Gaps 9;

QY 208 GFTYIGPGDRVACFACGKLSNWEKDDAMSEHRRHFPNCPFLNSLETFRS----- 260
DB 54 GPKYNOVDHVCCEAEATKMSDECEIYAHVTLSPYCAVANKIAEHESFGDNTINA 113
QY 261 -----ISNLSMOTHAARMTFM-YMPSSVVPVPEOLASAGFYVGRNDVK 305
DB 114 VLVEGRPKVCYRCMSNLQ-----SRMDTFVNFWPALRDMITNIAEAGLFYGRGDETV 168
QY 306 CFCCDGLRCWESGDDPVVHAKMPPRCPEFLIRMGQEFVDIETGRYPHLLLEQLSTSDT 365
DB 169 CFECDCVRDMHINEDAMQNHATEMPQCYFVLSVKKEFCQ----- 209
QY 366 TGEENADPPIHFGESSESDAVMNTPVYKSALEMGNKDLVQTVQSKILTGENYK 425
DB 210 ----- 209
QY 426 TVNDIVSALNAEDEKEEKEKQAEASDDLSLRKNRMALFQQLTFCVLPILDNLKA 485
DB 210 -----NAITATHVDKDD-----DD-----DNNLNE 232
QY 486 NVINKQEHDIKQKQIPLQARELIDTLLVKGNAANIFKNCKLEIDSTLYKNLFDVKM 545
DB 233 NV-----DDDI----- 238
QY 546 KIPTEDVSGLSLEQLRLQEEERCKVCMDKEYSVPIPCGHLVYCOECAPSL-RKCP 604
DB 239 -----EKEECKVCLEQRQDAVLMPCIRHFCVCQCYCFELDDKCP 278
QY 605 CRGIKGTVRTEL 617
DB 279 CRQDVATDFIKITV 291

RESULT 14
T43523
cut17 protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000
C:Accession: T43523; T41649; T41700
R:Morioka, J.; Matsusaka, T.; Yanagida, M.
Submitted to the EMBL Data Library, August 1999
A:Description: Fission yeast cut17 is required for chromosome segregation.
A:Reference number: 222536
A:Accession: T43523
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-997 <MOR>
A:Cross-references: EMBL:AB031034; PIDN:BA083415.1
R:Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, August 1998
A:Reference number: 222007

A:Accession: T41649
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-997 <HAR>
A:Cross-references: EMBL:AL031323; PIDN:CAA20434.1; GSPDB:GN00068; SPDB:SPCC962.02c
A:Experimental source: strain 972h-; cosmid c962
R:Medler, H.; Duisterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, October 1999
A:Reference number: 222010
A:Accession: T41700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 932-997 <MED>
A:Cross-references: EMBL:AL121859; PIDN:CAB58376.1; GSPDB:GN00068; SPDB:SPCP31B10.10c
C:Genetics:
A:Gene: cut17; SPCC962.02c; SPDB:SPCP31B10.10c
A:Map position: 3L
A:Introns: 43/3

Query Match 7.2%; Score 237.5; DB 2; Length 997;
Best Local Similarity 23.1%; Pred. No. 3.3e-08;
Matches 106; Conservative 63; Mismatches 196; Indels 93; Gaps 22;

QY 164 RAVEDISSSRNPYAMSTBEARFLTH--MPLTFLSPELARAGFY--IGPG----- 215
DB 2 KPISSSKRRNRRFRREMCYSKRLDTFOKKKMRBRAPETLATVGYNNPISSESS 61
QY 216 --DRVACFACGKLSNWEKDDAMSEHRRHFPNCPFLNSLETFRSISNLSMOTHA-- 271
DB 62 RLNDVTCYMCYKSFEDMEDDDPLKEHTHSPSCPW-----AYLSSKNNPNQNPQAAL 116
QY 272 ---RMRTFM--YMP-----SSVPVPEOLASAGFY--VGRNDVKCFCCDGLRCWESG 319
DB 117 TKCREQTFVQVWPTNRPDYHCEPSVMAASGFYNPADAKDAHCLYCDINLHMEPD 176
QY 320 DDPVWEHAKMPPRCPEFLIRMGQEFVDEIQRYPHLL-----QLSTSDTGE--NADPP 374
DB 177 DDPTYEHKRRRADCVF-----FTWKDPSLSPTKLSLSTNIDPEDLTEDNS 224
QY 375 IIFGEGSESDAVMAN-TPVVSALF-MGFNRDLVQTVQSK-----IL 418
DB 225 ILVPSPTROSTKSHKTLNFSPSRKNNLNARPLTWLSLYNTSEKDSQPTRAPQSPKPV 284
QY 419 TTGENYK-----TVNDIVSALNAEDEKEEKEKQ--AEEMASDDLSLRKNRMA 467
DB 285 LTAPRRKNKSPKSPKPAVFPVKPIFSDEDEDDDLTASQPSFGICNDMSQYAKKN--- 341
QY 468 LFQQLTFCVLPILDNLKANVINKQEHDIKQKQIPLQARELIDTLLVKGNAANIFKN 527
DB 342 ---FTEEIPLEKED---EKDNELEH-LVSPATSVHTTVSDTGHQSVTDESDEQ--NNC 390
QY 528 LK-----EIDSTLYKNLFDVKNMKYIPTEDVSGLSLEE 560
DB 391 MSTPKRIEISKEIEISVYSKSKKEI-SSSVSSVQKEQ 427

RESULT 15
D36828
orf13 protein - Autographa californica nuclear polyhedrosis virus
C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Nov-2000
C:Accession: D36828; C72853
R:Branaagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.
Virology 191, 1003-1008, 1992
A:Title: Sequence, genomic organization of the EcoRT-A fragment of Autographa californica
VP8 of rotavirus.
A:Reference number: A44221; MID:93079853; PMID:1333113
A:Accession: D36828
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <BRA>
A:Cross-references: GB:S52569
R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

Virology 202, 586-605, 1994

A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus

A:Reference number: A72850; MUID:94303173; PMID:9030224

A:Accession: C72853

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-199, 'L', 201-286 <AYR>

A:Cross-references: GB:L22858; NID:9510708; PIDN:AAA66657.1; PID:9559096

C:Genetics:

A:Gene: Ac-IAP1

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 7.2%; Score 235.5; IB 2; Length 286;
Best Local Similarity 17.6%; Pred. No. 7.3e-09;
Matches 83; Conservative 47; Mismatches 112; Indels 229; Gaps 11;

```
QY 173 RTNPYSYAMSTERARFLTYHMPL--TFLSPSELARAGFYIIGPGDRVACFACGGKLSN 229
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 RDMTAEHYFDMLIERHSSFENPIENTAFI--NSLIYNG:PKYNOYDDHVCCEYCEAEIKN 75
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 230 WEPKDAMSEHRRHFPNCPFLENSLETLRFS-----ISNLSMOT 268
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 WSEDECIYAHATLSPYCAVANKIAERESFGDNITINAVIYKEGPKCYVRCMSNLQ--- 132
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 269 HAARMRTFM-YMPSSVYQPEGLASAGFYVGRNDYKICCCDGLRCWESGDDPWVEHA 327
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 133 --SRMDTFVNFMPALRDMITNIAEAGLFTYGRGDETVCFCDCCVROMHTNEDTWQRHA 190
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 328 KMFPRCEFLIRMGQEFVDEIQGRYPHLLLEQLLSTSDTGEENADPPIIHFGPESSSED 387
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 AENPQCYFVXSVKKEFC----- 208
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 388 AVAMNTPVVKSALEMGNFNDLVKQTVOSKILTTGENYKTVNDIVSALLNADEKREEKE 447
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 209 -----ONSITVTHV-----DKRDD--- 222
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 448 KQAEEMASDDLILIRKNMALFQQLCVLPILDNLKANYNKQEHDIKQKTQIPLOAR 507
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 223 -----DNL-----NENADDI----- 232
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 508 ELIDTILVKGNAANIFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSLEQLRLQE 567
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 233 -----EE 234
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 568 EPTCKVCMDEKESVFIIPCGHLVVCQECAPSL-RKCPICRGIIKGTVRTFL 617
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 KYECKVCLERQDAVLMPCRHFCVCVQCIFGLDQKCPCTCRQDVTPFIKIFV 285
    | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: May 5, 2003, 16:08:04
Job time : 71.6382 secs

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 25.633 Seconds
(without alignments)
1000.040 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277
Sequence: 1 MKKTASQRLFPSPSYGNKLS.....LKKPCRCIGIKGVTRFLS 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3277	100.0	618	BIR3_HUMAN	Q13490 homo sapien
2	2728	83.2	612	BIR3_MOUSE	Q62210 mus musculu
3	2353	71.8	604	BIR2_HUMAN	Q13489 homo sapien
4	2233.5	68.2	611	BIR1_CHICK	Q90660 gallus galli
5	2172	66.3	600	BIR2_MOUSE	Q08863 mus musculu
6	1532	46.8	358	PIAP_PIG	Q62640 sus scrofa
7	911	27.8	497	BIR4_HUMAN	P98170 homo sapien
8	910	27.8	496	BIR4_MOUSE	Q60989 mus musculu
9	904.5	27.6	496	BIR4_RAT	Q91016 rattus norv
10	744.5	22.7	498	IAP2_DROME	Q24307 drosophila
11	513	15.7	268	IAP3_NPVOP	P41437 orgyia pseu
12	506	15.4	1403	BIRE_MOUSE	Q91016 mus musculu
13	499.5	15.2	1403	BIRF_MOUSE	Q911b6 mus musculu
14	498.5	15.2	1402	BIRG_MOUSE	Q911b3 mus musculu
15	484	14.8	438	IAP1_DROME	Q24306 drosophila
16	468.5	14.3	1403	BIRA_MOUSE	Q9qwk5 mus musculu
17	468	14.3	1447	BIRB_MOUSE	Q9qwk4 mus musculu
18	462	14.1	1403	BIR1_HUMAN	Q13075 homo sapien
19	461	14.1	275	IAP_GYCP	P41436 cydia pomon
20	460.5	14.1	298	BIR7_HUMAN	Q96cas5 homo sapien
21	459.5	14.0	236	BIR8_GORGO	Q95m71 gorilla gor
22	458.5	14.0	236	BIR8_HUMAN	Q96p09 homo sapien
23	457.5	14.0	236	BIR8_PANTR	Q95m72 pan. troglod
24	438.5	7.3	286	IAP1_NPVAC	P41435 autographa
25	237.5	7.2	997	BIR1_SCHPO	Q14064 schizosacch
26	223.5	6.8	275	IAP1_NPVOP	Q10296 orgyia pseu
27	199.5	6.1	4829	BIR6_HUMAN	Q9nro9 homo sapien
28	175.5	5.4	239	ZFP_IRV6	P47732 chilo iride
29	144	4.4	249	IAP2_NPVAC	P41454 autographa
30	141.5	4.3	142	BIR5_RAT	Q91hy7 rattus norv
31	139	4.2	140	BIR5_MOUSE	Q70201 mus musculu
32	137.5	4.2	236	IAP2_NPVOP	Q10324 orgyia pseu
33	132.5	4.0	490	MDM4_HUMAN	Q15151 homo sapien

34	131	4.0	142	1	BIR5_HUMAN	Q15392 homo sapien
35	126	3.8	145	1	ZEP2_IRV6	P40629 chilo iride
36	124	3.8	433	1	RN26_HUMAN	Q9by78 homo sapien
37	120.5	3.7	834	1	YNCA_CAEEL	P34537 caenorhabdi
38	120.5	3.7	954	1	BIR1_YEAST	P47134 saccharomyc
39	119.5	3.6	487	1	MDM2_CANFA	P56950 canis fam11
40	119.5	3.6	735	1	YDD7_SCHPO	Q10432 schizosacch
41	119	3.6	619	1	PRIA_HELPY	Q25149 helicobacte
42	116.5	3.6	3418	1	BIR2_HUMAN	P51587 homo sapien
43	116	3.5	624	1	YMO8_YEAST	P54074 saccharomyc
44	115.5	3.5	491	1	MDM2_HUMAN	Q00987 homo sapien
45	112.5	3.4	1075	1	PST2_SCHPO	Q13919 schizosacch

ALIGNMENTS

RESULT 1
BIR3_HUMAN STANDARD: PRT: 618 AA.

AC Q13490; Q16516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 2) (H1AP2) (H1AP2) (C-IAP1) (TNFR2-TRAF signaling complex protein 2) (IAP homolog B).
DE BIR3 OR API2 OR IAP2 OR MIH8.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96128127; PubMed-8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel E.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE-96149249; PubMed-8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE-96209843; PubMed-8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RA Strausberg R.;
RL Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.
RN [5]
RP STRUCTURE BY NMR OF 266-363.
RX MEDLINE-99332054; PubMed-10404221;
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat.";
RL Nat. Struct. Biol. 6:648-651(1999).
CC -I- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 ANT TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
 CC Inhibit apoptotic suppressor activity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
 CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
 CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
 CC LEUKOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- DATABASE: NAME-Atlas Genet. Cyogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BIRC3ID239.html".
 CC
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DR EMBL: L49431; AAC41942.1; -
 DR EMBL: U45879; AAC50372.1; -
 DR EMBL: U37547; AAC50508.1; -
 DR EMBL: BC016174; AAH16174.1; -
 DR PDB: 1QBH; 20-OCT-99.
 DR Genew: HGNC:590; BIRC2.
 DR MIM: 601721; -
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 3.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Apoptosis; Zinc-finger; Repeat; 3D-structure.
 DR KW Apoptosis; Zinc-finger; Repeat; 3D-structure.
 FT REPEAT 46 113 BIR 1.
 FT REPEAT 184 250 BIR 2.
 FT REPEAT 269 336 BIR 3.
 FT DOMAIN 453 543 CARD.
 FT ZN_FING 571 606 RING-TYPE.
 FT CONFLICT 157 157 S -> P (IN REF. 2).
 FT CONFLICT 308 308 C -> G (IN REF. 2).
 FT CONFLICT 414 414 Q -> L (IN REF. 2).
 FT CONFLICT 514 514 L -> W (IN REF. 2).
 SQ SEQUENCE 618 AA: 69899 MW: C1778D328063586E CRC64;

Query Match 100.0%; Score 3277; DB 1; Length 618;
 Best Local Similarity 100.0%; Pred. No. 6.5e-209;
 Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHKTASQRLFPSPQNIKIMEDSTILSDWTNKNKKYDSCSELYRMSTYTFAGV 60
 DB 1 MHKTASQRLFPSPQNIKIMEDSTILSDWTNKNKKYDSCSELYRMSTYTFAGV 60
 QY 61 PVSESLARAGFYTYGVNDKVKFCGGLMDNMKLGDSPIQIKIKOLYPSCSFTQNLVSAS 120
 DB 61 PVSESLARAGFYTYGVNDKVKFCGGLMDNMKLGDSPIQIKIKOLYPSCSFTQNLVSAS 120
 QY 121 LGSTNNTSPMRNSFAHSLSPLEHSLPFGSYSSLSPNPLNRAVEDISSRTNPYSYA 180
 DB 121 LGSTNNTSPMRNSFAHSLSPLEHSLPFGSYSSLSPNPLNRAVEDISSRTNPYSYA 180
 QY 181 MSTEARFLTYHMPDLTFLSPSEILARAGFYTYIGPDRAVACFACGKLSNWEPRDAMSEH 240
 DB 181 MSTEARFLTYHMPDLTFLSPSEILARAGFYTYIGPDRAVACFACGKLSNWEPRDAMSEH 240

DB 181 MSTEARFLTYHMPDLTFLSPSEILARAGFYTYIGPDRAVACFACGKLSNWEPRDAMSEH 240
 QY 241 RHHFPCPLENSLEFLRFESISNLSMOTHAARMRTFMYPPSSVPVQPOLASAGFYTYGR 300
 DB 241 RHHFPCPLENSLEFLRFESISNLSMOTHAARMRTFMYPPSSVPVQPOLASAGFYTYGR 300
 QY 301 NDDVKCFCCDGLRCWESGDDPWVHAKMPPRCEFLIRKKGQEFVDEIGRPHLEQLL 360
 DB 301 NDDVKCFCCDGLRCWESGDDPWVHAKMPPRCEFLIRKKGQEFVDEIGRPHLEQLL 360
 QY 361 STSDTGEENADPPIIHFGPESSEDAVMMNTPVKSALEMENRDLVKQVQSKILTT 420
 DB 361 STSDTGEENADPPIIHFGPESSEDAVMMNTPVKSALEMENRDLVKQVQSKILTT 420
 QY 421 GENKYRVNDIYSALNAEDEREKEKEQAEMASDDLSLRNRMAFQQLCVLPILD 480
 DB 421 GENKYRVNDIYSALNAEDEREKEKEQAEMASDDLSLRNRMAFQQLCVLPILD 480
 QY 481 NILKANVINKEHDIKQKQIPLQARELIDTILVKGNAANIFKNCLEISTLYKNLF 540
 DB 481 NILKANVINKEHDIKQKQIPLQARELIDTILVKGNAANIFKNCLEISTLYKNLF 540
 QY 541 VDKNMKYIPTEDVSGLSLEQLRLQOERTCKVCMDEKVSVPFIPCGHLVYCOECAPSLR 600
 DB 541 VDKNMKYIPTEDVSGLSLEQLRLQOERTCKVCMDEKVSVPFIPCGHLVYCOECAPSLR 600
 QY 601 KCPICRGIIKGTVPFELS 618
 DB 601 KCPICRGIIKGTVPFELS 618

RESULT 2
 BIR3_MOUSE STANDARD; PRT; 612 AA.

AC 062210; 008864;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
 protein 2) (MIAF2) (MIAF-2).
 GN BIRC3 OR API2 OR IAP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RX MEDLINE=96128127; PubMed=8548810;
 RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
 RT "The TNFR2-TRAF signaling complex contains two novel proteins related
 to baculoviral inhibitor of apoptosis proteins.";
 RL Cell 83:1243-1252(1995).
 RN [2]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=98110590; PubMed=9441758;
 RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
 RT "Genomic characterization of the mouse inhibitor of apoptosis protein
 1 and 2 genes.";
 RL Genomics 46:495-503(1997).
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
 CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
 CC Inhibit apoptotic suppressor activity (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
 CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC -----
DR EMBL: L49433; AAC42078.1;
DR EMBL: U88909; AAC53532.1;
DR HSSP: Q13490; 1QBH.
DR MGD: MGI:1197009; Birc3.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS0518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS0089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C10D CRC64;

Query Match      83.2%; Score 2728; DB 1; Length 612;
Best Local Similarity 83.4%; Pred. No. 1.1e-17;
Matches 517; Conservative 45; Mismatches 48; Indels 10; Gaps 6;

QY 1 MHKTAQRLEFPSPSYONIKSIMEDSTLSDWTNSNKKMYNFCSELYRMSTYSPFAGV 60
DB 1 MDKTVSQRIGOGTFLHOKLRIMKSTILSNMTKESEKMKPFSCELYRMSTYSAFPRGV 60

QY 61 PVSESLARAGFYTGVDVKVCECCGIMLDNMWKLGDSPIOKHOLYPSCEFIOMLVAS 120
DB 61 PVSESLARAGFYTGVDVKVCECCGIMLDNMWKLGDSPVEKHOPYPCSFVQTLISAS 120

QY 121 LGSRTSKNTSPMRNSFAHSLSPTEHSLFSGSYSSLSPLN3RAVEDISSRTNPSYA 180
DB 121 LQSPSKNMSPVKSRFAHS-SP-LEP-----GGIHSNLCSSPLNSRAVEDF-SSRMDPCSYA 173

QY 181 MSTEEARFLTYHMPLEFLPSSELRAGFYIIGPDVACFA;GGRKLSNMEPKDDAMSEH 240
DB 174 MSTEEARFLTYHMPLEFLPSSELRAGFYIIGPDVACFA;GGRKLSNMEPKDDAMSEH 233

QY 241 RRRHPNCPLENSLETLEFSESILSMOTHAARTEMWPSVVPVPEOLASAGFYVGR 300
DB 234 RRRHPNCPLENSLETLEFSESILSMOTHAARTEMWPSVVPVPEOLASAGFYVDR 293

QY 301 NDDVKCFCCDGLRCWEGSDDPVVEHAKWPRCEFLIRMGQEVVEIQGYPHLLQQL 360
DB 294 NDDVKCFCCDGLRCWEGSDDPVVEHAKWPRCEFLIRMGQEVVEIQGYPHLLQQL 353

QY 361 STSPTTEENADP--PIIHFGPESSSEDVAMNTPYVKSALDEMGFNRLVQYVOSKIL 418
DB 354 STSPTTEENADPPIETVYVHFGE--SSDDVYVAMSTPYKALEMGFSRSLVQYVORQIL 412

QY 419 TTGENYKTVNDIVSALNAEDEKREERKEKQAEASDDLILIKRNMALFOQLCVLP 478
DB 413 ATGENYRTVNDIVSVLNAEDERREERKEERQEMASGDLILIKRNMALFOQLTHVLP 472

QY 479 LDNLKANYINKOEHDITKQKQIPIQARELIDTILVKGNAANITKNCKLEIDSTLYKN 538

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DB 473 LDNLLEASVITKOEHDITKQKQIPIQARELIDTILVKGNAANITKNCKLEIDSTLYEN 532
QY 539 LFVYKNMKYIPTEDVSGSLSEQLRRIQOEERTCKVCMDEKYSVVFIPCGHIVVCCCAPS 598
DB 533 LFVEKNMKYIPTEDVSGSLSEQLRRIQOEERTCKVCMDEKYSVVFIPCGHIVVCCCAPS 592
QY 599 LRRCPICRGIKGVTRTFLS 618
DB 593 LRRCPICRGTIKGVTRTFLS 612

RESULT 3
BIR2_HUMAN
ID BIR2_HUMAN STANDARD; PRT; 604 AA.
AC Q13489; Q16628; Q9UP46; Q9HC27;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (inhibitor of apoptosis
DE protein 1) (HAPI) (HAP-1) (C-IAP2) (TNFR2-TNFR signaling complex
DE protein 1) (IAP homolog C).
GN BIRC2 OR API1 OR IAP1 OR MIRC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TNFR signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamel K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by Nalp and a related
RT family of IAP genes.";
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99252096; PubMed=10233894;
RA Horrevoets A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, stannin, and two novel
RT genes.";
RL Blood 93:3418-3431(1999).
RN [5]
RP SEQUENCE OF 362-441 FROM N.A.
RX MEDLINE=20519161; PubMed=11066071;
RA Baens M., Steyls A., Dierlam J., De Wolf-Peters C., Marynen P.;
RT "Structure of the MTR gene and molecular characterization of the
RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
RT B-cell lymphomas of MALT type.";
RL Genes Chromosomes Cancer 29:281-291(2000).
CC -I- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

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[illegible]

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0Y      20 S1MEDST1LSDMTNS-NKOKMKYDFSCELYRMSYSTFEPAGVFSERSLARAGFYTTGVN 78
      ::::| |:-| |::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2 N1VENST1FLSNLMKXSANTFELKYDLCSELYRMSYSTFEPAGVFSERSLARAGFYTTGVN 61

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RESULT 4			
ID	BIR_CHICK	STANDARD;	PRT; 611 AA.
AC	090660;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis protein).		
DE	ITA.		
GN	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Spleen;		
RA	MEDLINE=97101112; PubMed=8945639;		
RA	Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;		
RT	"ITA, a vertebrate homologue of IAP that is expressed in T lymphocytes.";		
RT	DNA Cell Biol. 15:981-988(1996).		
CC	-1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.		
CC	-1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.		
CC	-1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF T-CELL ACTIVATION IN SPLEEN AND THYMUS.		
CC	-1- SIMILARITY: BELONGS TO THE IAP FAMILY.		
CC	-1- SIMILARITY: CONTAINS 3 BIR REPEATS.		
CC	-1- SIMILARITY: CONTAINS 1 CARD DOMAIN.		

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CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27466; AAB48118.1; -
DR HSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS00143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; Nuclear protein.
FT REPEAT 30 97 BIR 1.
FT REPEAT 176 242 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 446 536 CARD.
FT ZN_FING 564 599 RING-TYPE.
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;

Query Match 68.2%; Score 2233.5; DE 1; Length 611;
Best local similarity 69.2%; Pred. No. 4.6e-140;
Matches 424; Conservative 77; Mismatches 95; Indels 17; Gaps 8;

QY 20 SIMESTILSDWTSNKQ--KMYDFSCGLYRMSTYFPAQVPSRSLARAGFYTG 77
Db 2 NIMOSPLASVKNAMHAGELKYDFSCGLYRMSTYFPAQVPSRSLARAGFYTG 61
QY 78 NDKYKFCGGLMDNWKGLDSPLOKHQOLYPCSFIONLVSA-SLG-ST-----SKN 127
Db 62 QDKYKFCGGLVLDNMQGDNAEKHKQYPPSCSFYQNMLSNLTGSHAFSPVLASN 121
QY 128 TSPMNSFAHSLPTLEHSSLSFGSYSSLSNPPLNSRAVEDYSSRTNPYSYAMSTEAR 187
Db 122 LSPSLRSM--TLSPSEFOYGYEGSFSFPRDPVYTRAEDI.SHLNKLQNPMSSTEER 179
QY 188 FLTYHMPFLTFLSPSELARAGFYIIGPDRAVACFACGKLSNMPKDDAMSEHRRFPNC 247
Db 180 LRTSHAMPFLMCLMVAEVAAGLDLGTADKACVNCGVKLSNMPKDDAMSEHRRFPNC 239
QY 248 PFLNSL-ETLRFSISNLSMOTAAARMTFTWPSVYVQPEQLASGFYVGRNDVKC 306
Db 240 PVENLMRDQPSFVSNVYMTQTEARVYKTFIMWPTRIPVQPEQLADAGFYVGRNDVKC 299
QY 307 FCCGGGLRCWESGDDPWVEHAKWPRCEFLIRNKGQEFVDEIGRYPHLL- EQLSTSDT 365
Db 300 FCCGGGLRCWESGDDPWVEHAKWPRCEFLIRNKGQEFVSOYQARPHLLMNSCTSDK 359
QY 366 TGEENADPPIIHFGPSSSESDAVMMNTPVVKSALFMGFNRPDLVKOTVQSKILTGENYK 425
Db 360 PVDENMD-PIIHFGPSSSESDAIMNTPVVKALEMGFSRRILKOTVQSKILAEENYK 418
QY 426 TVNDIVSALLNAEDEKREKEKEQAEEMASDLSLRKNRMALFOQLTCVPIIDMLIKA 485
Db 419 TVNDIVSELTADEKREKEKEQAEEMASDLSLRKNRMALFORLTSLVPIILGLLSA 478
QY 486 NVINKQEHIIKQTOIPLQARELIDITLVKGNAAANIFKNCIKEIDSTLYKNLFYDKNM 545
Db 479 KVITELHGVYIKQTOIPLQARELIDITLVKGNAAANIFKNCIKEIDSTLYKNLFYDKNM 538

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QY 546 KIYPEDVSGLSLEQLRLQEEETCKVCMDEKSVYVFI PCGHLVYVCEQCAPSLRKCPC 605
Db 539 KIYPEDVSGLSLEQLRLQEEETCKVCMDEKSVYVFI PCGHLVYVCEQCAPSLRKCPC 598
QY 606 RGIINGTVRFLS 618
Db 599 RGIINGTVRFLS 611

RESULT 5
BIR2_MOUSE
ID BIR2_MOUSE STANDARD; PRT: 600 AA.
AC 008653;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (inhibitor of apoptosis
DE protein 1) (M1AP1) (M1AP-1).
GN BIRC2 OR API1 OR IAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROOMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL: U88908; AAC53531.1; -
DR HSP: Q13490; 1QBH.
DR MGI: I197007; Birc2.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS00143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 27 94 BIR 1.
FT REPEAT 167 233 BIR 2.
FT REPEAT 253 320 BIR 3.

```

FT DOMAIN 436 525 CARD.
 FT 2N_FING 553 588 RING-TYPE.
 SQ SEQUENCE 600 AA; 67198 MW; AD7F73E6849317D1 CRC64;

Query Match 66.3%; Score 2172; DB 1; Length 600;
 Best Local Similarity 66.7%; Pred. No. 5.1e-136;
 Matches 406; Conservative 87; Mismatches 96; Indels 20; Gaps 7;

QY 21 IMEDSTILSDWTNS-NKOKMYDFSCELYRMSTYSTPAGVPYSESRSLARAGFYTGND 79
 Db 1 MYODSAFLAKLMKSAADTFELKYLSTYSAFPGVPSERSLARAGFYTGND 60.
 QY 80 KYKFCGGLMDNWKIGDSPQKHQOLYPSCSFTONLSA-----SLGTSKATSP 130
 Db 61 KYKFCGGLMDNWKIGDSPQKHQOLYPSCSFTONLSA-----SLGTSKATSP 120
 QY 131 MNSEFASLSPTLEHSSLSFSGSYSLSPNLSRAVEDISSRTNPTYSAMSTEARFL 190
 Db 121 L--SFSS-----ENMGFSSSYSPSPDPVNFANODCVALSTSPHYAMNTEKARLT 173
 QY 191 YHMPPLFLSPSELARAGFYIIGPDVACFACGKLSNMEPKDDAMSEHRRHPNCPFL 250
 Db 174 YETWPLSFLSPAKLAKAGFYIIGPDVACFACGKLSNMEPKDDAMSEHRRHPNCPFL 233
 QY 251 EN-SLETRFSISNLSMOTHAARMTFMTWPSVYQPEGLASAGFYVGRNDVKRC 309
 Db 234 KDLGOSASRYTVSNLSMOTHAARMTFMTWPSVYQPEGLASAGFYVGRNDVKRC 293
 QY 310 DGLRCWESGDDPWVHAHAKFPRCEFLIRKKGQEVDEIQGRYPHLEQLSTSDTGE 369
 Db 294 DGLRCWESGDDPWVHAHAKFPRCEFLIRKKGQEVDEIQGRYPHLEQLSTSDTGE 353
 QY 370 NADPPIHFGESSESDAVMNTPVYKSALEMGNRDLVKQVOSKILTTGENYKTVND 429
 Db 354 NADPPIHFGESSESDAVMNTPVYKSALEMGNRDLVKQVOSKILTTGENYKTVND 412
 QY 430 IYSALNAEDEKEREKEKQAEEMASDDLIRKRMALFQQLCVLPILNLLKANYIN 489
 Db 413 IYGLDAEDEMREEMQAEESDDLIRKRMALFQQLCVLPILNLLKANYIN 472
 QY 490 KOEHDIKOKQIPLARELIDTILVKGNAANIFKNCLKIDSTLYKNLFLVKNMKYIP 549
 Db 473 EOCNMAVOKQPR-TLOASTLIDTILVKGNAANIFKNCLKIDSTLYKNLFLVKNMKYIP 531
 QY 550 TEVSGSLSEQLRLQOEERCKVCMDKEYSVFIPCGHLVCOECAPSLRKCPICRGTI 609
 Db 532 TDIDIALPMEBQLRKQOEERCKVCMDKEYSVFIPCGHLVCOECAPSLRKCPICRGTI 591
 QY 610 KGTVRTFLS 618
 Db 592 KGTVRTFLS 600

RESULT 6
 ID PIAP_PIG STANDARD; PRT; 358 AA.
 AC 062640;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative inhibitor of apoptosis.
 GN PIAP.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=98162622; PubMed=9501011;
 RA Stehlik C., de Martin R., Binder B.R., Lipp J.;
 RT "Cytokine induced expression of porcine inhibitor of apoptosis
 protein (Iap) family member is regulated by NF-kappa B.";

RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U79142; AAC39171.1; .
 DR HSP: Q13490; IQBH.
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00653; BIR; 2.
 DR SMART: SM00238; BIR; 2.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS0143; BIR_REPEAT_2; 2.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR KX Apoptosis; Zinc-finger; Repeat.
 FT REPEAT 4 70 BIR 1.
 FT REPEAT 90 157 BIR 2.
 FT DOMAIN 193 283 CARD.
 FT 2N_FING 311 346 RING-TYPE.
 SQ SEQUENCE 358 AA; 40977 MW; EB226BFA9A6190A4 CRC64;

Query Match 46.8%; Score 1532; DB 1; Length 358;
 Best Local Similarity 65.1%; Pred. No. 4.3e-94;
 Matches 286; Conservative 38; Mismatches 33; Indels 82; Gaps 2;

QY 181 MSTEARFLTYHMPPLFLSPSELARAGFYIIGPDVACFACGKLSNMEPKDDAMSEH 240
 Db 1 MNTKRLTLTQMWPLFLSPADLAKAGFYIIGPDVACFACGKLSNMEPKDDAMSEH 60
 QY 241 RHRFPNCFLENSL-ETLRFSISNLSMOTHAARMTFMTWPSVYQPEGLASAGFYTG 299
 Db 61 LRHFPNCFLENSL-ETLRFSISNLSMOTHAARMTFMTWPSVYQPEGLASAGFYTG 120
 QY 300 RNDVAKCFCCDGLRCWESGDDPWVHAHAKFPRCEFLIRKKGQEVDEIQGRYPHLEQL 359
 Db 121 HSDVAKCFCCDGLRCWESGDDPWVHAHAKFPRCEFLIRKKGQEVDEIQGRYPHLEQL 180
 QY 360 LSTSDTTGEENADPPIHFGESSESDAVMNTPVYKSALEMGNRDLVKQVOSKILT 419
 Db 181 LSTSDNEDENAEPP-----NDLSLRKNMALFQHLTCVLPIL 195
 QY 420 TGENYKTVNDIVSALNAEDEKEREKEKQAEEMASDDLIRKRMALFQQLCVLPIL 479
 Db 196 -----NDLSLRKNMALFQHLTCVLPIL 219
 QY 480 DNLLKANVINKEHDIKOKQIPLARELIDTILVKGNAANIFKNCLKIDSTLYKNL 539
 Db 220 DNLLKANVINKEHDIKOKQIPLARELIDTILVKGNAANIFKNCLKIDSTLYKNL 279
 QY 540 EYDKNNKIIPEDVSGSLSEQLRLQOEERCKVCMDKEYSVFIPCGHLVCOECAPSL 599
 Db 280 EYODIKIIPEDVSGSLSEQLRLQOEERCKVCMDKEYSVFIPCGHLVCOECAPSL 339
 QY 600 RRCPIRGIIKGTVRTFLS 618
 Db 340 RRCPIRGIIKGTVRTFLS 358

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RESULT 7
BIR4_HUMAN
ID BIR4_HUMAN STANDARD; PRT; 497 AA.
AC P98170; O9N014;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP-like protein) (HILP).
OS BIR4 OR API3 OR IAP3 OR XIAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Balid S., Chertton-Horvat G.,
RA Parranani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal heart;
RX MEDLINE=96256286; PubMed=8654366;
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
RA Giffillan M.C., Shieles H., Hardwick J.M., Thompson C.B.;
RT "A conserved family of cellular genes related to the baculovirus iap
RT gene and encoding apoptosis inhibitors.";
RL EMBO J. 15:2685-2694(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Grafham D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE=97373959; PubMed=9230442;
RA Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;
RT "X-linked IAP is a direct inhibitor of cell-death proteases.";
RL Nature 388:300-304(1997).
RN [5]
RP MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.
RX MEDLINE=21634829; PubMed=11604410;
RA Verhagen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.,
RA Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L.,
RA Sampson R.J., Vaux D.L.;
RT "Hra2 promotes cell death through its serine protease activity and
RT its ability to antagonize inhibitor of apoptosis proteins.";
RL J. Biol. Chem. 277:445-454(2002).
RN [6]
RP STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.
RX MEDLINE=21020961; PubMed=11140637;
RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.,
RA Herrmann J., Wu J.C., Fesik S.W.;
RT "Structural basis for binding of Smac/DIABLO to the XIAP BIR3
RT domain.";
RL Nature 408:1004-1008(2000).
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.

```

	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC	-----
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CC	-----
DR	EMBL; U45880; AAC50373.1; -
DR	EMBL; U32974; AAC50518.1; -
DR	EMBL; ALI21601; CAB95312.1; -
DR	PDB; 1G3F; 10-JAN-01.
DR	GeneW; HGNC:592; BIRC4.
DR	MIM; 300079; -
DR	InterPro; IPR001370; BIR.
DR	InterPro; IPR001841; Znf_ring.
DR	Pfam; PF00097; zf-C3HC4; 1.
DR	Pfam; PF00653; BIR_3.
DR	SMART; SM00238; BIR; 3.
DR	SMART; SM00184; RING; 1.
DR	PROSITE; PS01282; BIR_REPEAT_1; 3.
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.
DR	PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR	PROSITE; PS50089; ZF_RING_2; 1.
KW	Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;
KW	3D-structure.
FT	REPEAT 26 93 BIR 1.
FT	REPEAT 163 230 BIR 2.
FT	REPEAT 265 330 BIR 3.
FT	ZN_FING 450 485 BIR 3.
FT	MUTAGEN 214 214 RING-TYPE.
FT	MUTAGEN 314 314 D->S: REDUCED INTERACTION WITH PRSS25.
FT	E->S: DECREASED INTERACTION WITH SMAC AND
FT	WITH PRSS25.
SQ	CONFLICT 162 162 S -> C (IN REF. 1).
FT	CONFLICT 423 423 Q -> P (IN REF. 2).
SEQUENCE	497 AA; 56684 MW; 9D394C16D45B635 CRC64;
Query Match	27.8%; Score 911; DB 1; Length 497;
Best Local Similarity	33.8%; Pred. No. 6.4e-53;
Matches 205; Conservative	89; Mismatches 163; Indels 150; Gaps 14;
QY	NKOKMKTDPSCELYRMSTYSTTPAGVPVYSERSLARAGYYTYGVNDKKYCFCCGLATDMWK 94
Db	18 NKEE---EFVEENRLKTFANPFGSGSPVASLATRAGLYTGSDGYVCFSCHAAYDMQ 74
QY	LCDSPIQKHQLYPCSFRIQNLIVASISLGTSKNTSPMRNSF-AHSLSPTEHNSLSFGSY 153
Db	75 YGDSSAVGRHKRVSPNCRIFNGFLSNSATQSTNSGIQGYKYENYLGSRDHLADRS- 133
QY	SSLSPNPINSRAVEDISSRTNPNYSYAMSTEAREFLTYHMWP-LTLFSPSELARAGFYI 212
Db	134 ETHADYLLRTGOVVDISDT-IYPRNPAMYSEEARLKSPQNMPDYAHLTPRELASAGLYTT 192
QY	GQGDRAVFACGCKLSNWEPKDDAMSEHRHPNCPFL-----EN 252
Db	193 GIGDOVOCCFCGCKLKMEPCBRAMSEHRRHFENCFFVLGRNLNIRSEDAVSSIDRNFPN 252
QY	SLETLRPSISNLMSQTHARMRTFMYPSSVPVQPEOLASAGYYVGANDDVKCFCCGG 312
Db	253 STLPLR----NPMAVDYAIRIFPGTWIYS--VNKEQLARAGFYALGSGDKVKCFHGCG 306
QY	LRCWESGDDPVWEHAKWPPRCEFLIRMGQEFVDEIOGRYPILLEQ-LLISTDTGEENA 371
Db	307 LIDMKPSSDPMECHAKRYPGCKYLLEQGQEYINNIT--HLTHSLECLVRTTEKT----- 359
QY	DPIIHFGPGSESSEDAAVMNTPVVKSALEMGNRDLIKOTVSKILLTGENKTVNDIV 431
Db	360 -----PSLTRRIDPTIFONPMWOEATIRMGSFSFKDKLIKMEKIQTIGSNKSLEYLV 411
QY	SALLNAEBEKREEKEQAEEAASDDLIRKRMLAEQOLTVCPLPIDNLKANVIKQ 491

Db 412 ADLVNACKDSMODE-----425
QY 492 EHDIIKQKTOIPLQARELIDITLVKGNAAANIFKNCLKEIDSTLYKNLFVDKMKIPIPE 551
Db 426 -----SSQTSIQLQ-----KIP-----435
QY 552 DVSGLSLEQLRLQERTCVCMKEVSVFIPCGHLVVCQECAPSLKRCPIRCGIITKG 611
Db 436 -----STEEQRLRLQERKLCIKCMBRNIAIVFVPCGHLVTCCKQCAEAVDKCPMCYVITFE 490
QY 612 TVRTFPLS 618
Db 491 KOKIFMS 497
RESULT 8
BIR4_MOUSE
AC 060989; STANDARD; PRT; 496 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP) (MIAP-3).
GN BIRC4 OR API3 OR XIAP OR AIP4 OR MIRA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors."
RT Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Farahant R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9 (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SMAC and PRSS25 are mediated by the second and third BIR domains (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL; U36842; AAC52594.1; -;
DR EMBL; U88990; AAB58376.1; -;
DR HSSP; Q13490; IQBH.
DR MGD; MGI:107572; Birc4.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; ZnF_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00553; BIR; 3.
DR SMART; SM00238; BIR; 3.

DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
FT FT 208 208 E -> K (IN REF. 2).
FT FT 317 317 E -> D (IN REF. 2).
FT FT 322 322 W -> C (IN REF. 2).
FT FT 346 346 S -> P (IN REF. 2).
FT FT 360 360 S -> P (IN REF. 2).
FT FT 388 388 I -> L (IN REF. 2).
FT FT 449 449 C -> S (IN REF. 2).
FT FT 462 462 V -> F (IN REF. 2).
FT FT 468 468 V -> A (IN REF. 2).
FT FT 490 490 K -> N (IN REF. 2).
SQ SEQUENCE 496 AA; 56079 MW; EC5FAE0799F2CDD8 CRC64;

Query Match 27.8%; Score 910; DB 1; Length 496;
Best Local Similarity 32.5%; Pred. No. 7.4e-53;
Matches 203; Conservative 92; Mismatches 156; Indels 174; Gaps 14;

QY 27 ILSDWTNSKQMKYDESCELYRMSTYFPAQVYSERSILARAGFYTGVDKVKFC 86
Db 13 VLAD---TNKDE--EFVEEFNRLKTFANFPSSPSVSASTLAGFLYTGEDTVQCFSC 66
QY 87 GLMDWKKLGDSPIQKHKOLYPSGFIQNLVSAISLGSISKNTSPMRNSFAHSISPTI 146
Db 67 HAAIDRWQYGDGSAVGRHRRISPCNRFI-----NGFYFENGAQSTNPQIONG 113
QY 147 SLFS---GSYSLSPNP-----LNSRAYEDISSRTNRYSIAMSTEARFPLYHM 193
Db 114 QYKSEKCVGNPNFAPDRPETHADYLLRTGQYVIDST-IYRNPAMCSEARLAKFQ 172
QY 194 WFLFPLSPSELARAGFYIYIGPDGVACFAGGKLSNNEPKDDAMSEHRKHPNCP 250
Db 173 WPDYAHITPRELASAGLYTGADDOVQCCGCKLENNEPCDAMSEHRKHPNCP 232
QY 251 -----ENSLFTLRFISINLSMOTHAARMRTMYWPSVPQPEOLASA 293
Db 233 RNWVRSESGVSDRNPSTNSPR---NPMAEYEARIVFTGWSS--VNKEOLARA 286
QY 294 GFYVGRNDVYKFCPCDGGRLRWESGDDPVYEHAKWFRCEFLIRMGQEFDEIGRYP 353
Db 287 GFYALGEGDKVCKFCGCGGLDMKPSDEPWEGHAKWYGCCKYLLDEKGOEYINNI 341
QY 354 HLEQLLSTSDTGEENADPPIIHFGPGESSSEDAVMNTPVYKSALEMGNRLVQ 413
Db 342 HLTHSLAESLGRTAET-----PSLTAKIDDTITONPMVOEALRMGSEFKDIK 392
QY 414 QSKILFTGENYKTVNDIVSALNADEKREKEKQAEEMASDDLSIRKNRMALEFQ 473
Db 393 EEKIOTSGSSYSLSLVLIADLVSAOKDNTDE----- 424
QY 474 CVLPILDNLKANVINKQEHDIQKTOIPLQARELIDITLVKGNAAANIFKNCLKE 533
Db 425 -----SSQTSIQLQ----- 431
QY 534 TLVKNLFDVKNMKIYPTEDVSGLSLEQLRLQERTCVCMKEVSVFIPCGHLVVC 593
Db 432 -----KDISTEEQRLRLQERKLCIKCMBRNIAIVFVPCGHLVTCCK 471
QY 594 ECAPSLKRCPIRCGIITKGTVRTFPLS 618
Db 472 QCAEAVDKCPMCYVITFEKOKIFMS 496
RESULT 9
BIR4_RAT

ID BIR4_RAT STANDARD: PRT: 496 AA.
AC Q9R016;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP) (IAP homolog A) (RIAP3) (RIAP-3).
DE (IAP homolog A) (RIAP3) (RIAP-3).
GN BIR4 OR API3 OR XIAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Salto N.;
RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9 (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SMAC and PRSS25 are mediated by the second and third BIR domains (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: AB033366; BAA85304.1; -
DR HSSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SMO0238; BIR; 3.
DR SMART: SMO0184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
SQ SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;
Query Match 27.6%; Score 904.5; DB 1; Length 496;
Best Local Similarity 33.2%; Pred. No. 1.7e-52;
Matches 206; Conservative 86; Mismatches 155; Indels 173; Gaps 15;
QY 33 NSNKKMKYDFSCSELYRMSTYTPAGVVSERSLARAGFYTYGVNDKVCFCGGLMDN 92
DB 16 DTKNDE--EFVEENRRLKTFANPPSSSVASATLARGFLTYGEGDTVQCSCHAAYDR 72
QY 93 WKLGSDPIOKHKLXPSCSFIONLYSASLGSTSKNTSP-----MRNSPAHS 138
DB 73 WQYGSAGVGRHRRISPCRFINGFYFEN-GAT-QSTSGIQNQYKSGENCVGNRNHA-- 128
QY 139 LSPTEHSLFSGSSLSLNPPLNSRAVEDISSRTNRYSTANSTEARFLTYHAMP-LT 197
DB 129 ---LDRPSETHADYL-----LRTGQVYDISDT-LYRNPANPCSEARLKTFTQNPDYA 177

QY 198 FLSPSELARAGFYIIGPDRVACGCKLSNMPEKDDAMSEHRRHPNCPRL----- 250
DB 178 HLSPRELASAGLYTGTIDQVQFCGCKLKNWPCDRAWSERRRRHPNCFVLGRNVN 237
QY 251 -----ENSLFTLRFSLNSMGTAAARMFTFMWSSVVPQPEOLASAGFYV 298
DB 238 RSESGVSSDRNFPNSTNSPR-----NPAAEYDARIYVFTGLYS--VNKEQLARAGFYAL 291
QY 299 GRNDVYKCFCCDGLRCWESGDDPWEHAKWPPRCFELIRMGQEFYDEIGRYPHLEQ 358
DB 292 GEGDVYKCFHCGGGLTWDKPSSEDPWEQAKWYPCCKYLLDEKGQETLNNI-----HLTHS 346
QY 359 LLTSDTGTGENADPPIIHFGPGSSSDAVMNTPVYKSALEMGRDLVKQTVOSKIL 418
DB 347 LGESVVRTAEKT-----PSYTKKIDDTITONPMVOEAIKMGFNFKDKITMEKQLQ 397
QY 419 TTGENYKTVNDIVASALNAEDEKREKEKEQAEMASDDLIRKNMALFOQLFCVLP 478
DB 398 TSGSNVLSLEVLADIADLVSAQKDNQDE----- 424
QY 479 LDNLKANVINKQEHDIKQKTOIPLQARELIDTILVKGMAANIFKNCLEIDSTLYKN 538
DB 425 -----SSQTSLQ----- 431
QY 539 LEVDKMKYIPTEVYSLGLEOLRLQERCKVKMDKEVSVFIPGHLVYCCQCAPS 598
DB 432 -----KDISTEQLRLQEKLCCKMDRNIAIVFVCGHLVTCQCAEA 476
QY 599 LKCPICRGILIKGTVTFLS 618
DB 477 VDKCPMCCFTVITFKQIFMS 496
RESULT 10
ID IAP2_DROME STANDARD: PRT: 498 AA.
AC Q24307; Q24177; Q24115; Q24149; Q9V7GL;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis 2 inhibitor (inhibitor of apoptosis 2) (DIAP2) (DIAP) (IAP homolog A) (IAP-like protein) (DILP).
GN IAP2 OR ILP OR DIHA OR CG8293.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE-Eye imaginal disk.
RX MEDLINE=96128128; PubMed=8548811;
RA Hay B.A., Wasserman D.A., Rubin G.M.;
RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins function to block cell death.";
RL Cell 83:1253-1262(1995).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE-Embryo;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., MacKenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN-Canton-S;
RX MEDLINE=96256286; PubMed=8654366;
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L., Gilliland M.C., Shiels H., Hardwick J.M., Thompson C.B.;
RT "A conserved family of cellular genes related to the baculovirus iap

RT gene and encoding apoptosis inhibitors.";
RL EMBL J. 15:2685-2694(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Cancon-S;
RL Ross J.L.;
RN Thesis (1991), Vanderbilt University / Nashville, U.S.A.
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Baller R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Foslter C., Gabriellian A.E., Garb N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[6]
RP SEQUENCE OF 17-498 FROM N.A.
RC TISSUE=Larva;
RX MEDLINE=96209843; PubMed=8643514;
RA Cren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND
CC HTD-DEPENDENT CELL DEATH IN THE EYE.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS THROUGHOUT
CC DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL: L49441; AAC41610.1; -
DR EMBL: U45881; AAC46988.1; -
DR EMBL: U32373; AAC47155.1; -
DR EMBL: M9581; -; NOT_ANNOTATED_CDS.
DR EMBL: AE003809; AAF58095.1; -
DR EMBL: U38809; AAB08398.1; -
DR HSSP: Q13490; 1QBH.
DR FlyBase: FBgn0015247; Iap2.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat.
KW REPEAT
FT REPEAT 9 76 BIR 1.
FT REPEAT 113 179 BIR 2.
FT REPEAT 212 279 BIR 3.
FT ZN_FING 451 486 RING-TYPE.
FT CONFLICT 5 5 G->V (IN REF. 2).
FT CONFLICT 40 40 N->K (IN REF. 2).
FT CONFLICT 64 65 ER->AG (IN REF. 3).
FT CONFLICT 94 94 E->K (IN REF. 1).
FT CONFLICT 282 282 A->S (IN REF. 6).
FT CONFLICT 286 286 A->S (IN REF. 3).
FT CONFLICT 302 302 P->Q (IN REF. 2 AND 5).
FT CONFLICT 303 303 P->T (IN REF. 6).
FT CONFLICT 327 327 A->T (IN REF. 2).
FT CONFLICT 369 376 ALVEYREP->DMRCASR (IN REF. 3).
SQ SEQUENCE 498 AA; 54506 MW; 66EC36DA6ED24AD6 CRC64;

Query Match 22.7%; Score 744.5; DB 1; Length 498;
Best Local Similarity 30.8%; Pred. No. 6.2e-42;
Matches 182; Conservative 85; Mismatches 206; Indels 117; Gaps 16;

OY 46 ELYRSTYSPFAGVPSERSLAAGFYTGVDKVCFCGCGMLDMWKLGRSPICKHQ 105
DB 9 ESVRLATFGWPLNAPVSAEDLVANGFATGNMLEACHFCHVRIDREYEGQVAERHR 68
OY 106 LYPSCSFIONLVASLSGTSKNTSPMRNSFAHSLSPTEHSLFSGSYSSLPNLSRA 165
DB 69 SSPICSMV--LAPNCGNPR-----SQESDNEGSS-- 97
OY 166 VEDISSRTNPYSAMSTEERAFITYHMWPLTFPSSELRAGFYIGPGRVACFACGG 225
DB 98 VVDSPESSCP--DLLEARNRLVFKDWPNNPITPOLAKAGFYINRLHVKCYWCNG 154
OY 226 KLSNWEKDDAMSEHRHFPNCPLE-----NSLETIRFSTISNLSMOTH--AA 271
DB 155 VIAKWEKNDNAFEEHRRFPQCPVOMGPLIERATGKNLDELGIQPTPLPLRPKYACVDA 214
OY 272 RMRITWYWPSSVPQP--EOLASAGFYVGRNDVKKFCDCDGLRCWESGDDPWEAKWKF 330
DB 215 RLRTFTDWPIS--NIQPASALAGALYYKIGDQVRCFCNIGRSMQKEDDEWFHAKWS 273
OY 331 PRCEFLIRMGQGEVDEIQRYPHLEQLLSTDSDTGEMADPPIIFGFGSSSSSDAVM 390
DB 274 PKQGVLLAKGPAYSEVLA-----TTAANASSPAP--APAPTLVADVLN 317
OY 391 MNTPVKSALEMGFRDLVKQTVOSKITLTGENYKTVDIYSALNNADEKREEKEKOA 450
DB 318 DEAP-AKALALGIDGVVARNALQKLLSSGCAFTIDELHDFDAGAGALEVREPP 376
OY 451 EEMASDDLILRKNMALFOQLFVPLIDNLKANVINKQEHDIKQTOPL--QARE 508
DB 377 EPSA---PTEPCQATTSKAASVPIVADS-----IPAKQAAE 412
OY 509 LIDTILVKGNAANIFKNCLKEIDSTLYKNLFDVCKNMKIIPTEDEVSGLSLEQLRLQEE 568

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DB 413 -----AVANISK-----ITDEIQKMYATPNNGNLSDEENRQKKA 448
QY 569 RICKVCADKEVSVEFIPCGHLVCCOECAPSIRKPCICRG:IKGTVRTFLS 618
DB 449 RLCKVCIDEVEGVFLPCGHLCATCNCAPSVANCPCMCRAIKGFVRTFLS 498

RESULT 11
ID IAP3_NPVOP STANDARD; PRT; 268 AA.
AC P41437;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis inhibitor 3 (IAP-3).
GN IAP3 OR IAP.
OS Orygia pseudotsugata multicapsid polyhedrosis virus (OPMPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=164623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94187094; PubMed=8139034;
RA Birnbaum M.J., Clem R.J., Miller L.K.;
RT "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polypeptide with Cys/His sequence motifs."
RL J. Virol. 68:2521-2528(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97271300; PubMed=9126251;
RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
RA Rohrmann G.F.;
RT "The sequence of the Orygia pseudotsugata multinnucleocapsid nuclear polyhedrosis virus genome."
RL Virology 229:381-399(1997).
CC -1- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY PREVENTING VIRAL STIMULATION OF APOPTOSIS.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
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CC
DR EMBL: L22564; AAB02610.1; -
DR EMBL: U75930; AAC59034.1; -
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 18 84 BIR 1.
FT REPEAT 111 178 BIR 2.
FT ZN_FING 221 256 RING-TYPE.
SO SEQUENCE 268 AA; 30076 MW; DF89175FDE85A708 CRC64;
QY 181 MSTEAFARFLTYHMMPLFLSPSELRAGFYIIGPDVRVACGCKLSMWEKDDAKSEH 240

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DB 15 MNKKAALGTTINWPOFLERSMAASGFYTLGRGDEVCAFCVETINIVRGDDPEIDH 74
QY 241 RHPFNPCEFLNSLE-----TLRFISNLSMOTHAARMRTFMWPSVPOFEOLAS 292
DB 75 KRWAPQCEPVRNNADHTPHDRAPPARSAAHPOVATEAARLTRAEWPGCLKORPEELAE 134
QY 293 AGFYVGRNDVCKFCFODDGLRCWESGDOPVEHAKWFPCEFLIRMGQEFVDEIQRY 352
DB 135 AGFEYTGQDKTRCFCCDGGHLDWEPDDAPWQHARWYDRCVEYLLVKGDFYOR----- 189
QY 353 PHLEQLISTSDTGTGENADPTIHFPGSSSSSDAVMMNTPVVKSALFMGFNDLVKQT 412
DB 190 -----VMEACVVR----- 198
QY 413 VQSKILTGENYKTVNDIVSALLNADEKREKEKQAEEMASDDLIRKNMALFOOL 472
DB 199 -----DADNEPHIERPAVEAE----- 214
QY 473 TCVLPIDLNLKANVINKQEHDIQKQTQIPLOARELIDTILVKGNAANIFKNCLKRID 532
DB 215 ----- 214
QY 533 SLLYKNLFVDKNMKYIPTEDVSGLSLEQIRLQERTCKVCADKEVSVEFIPCGHLVVC 592
DB 215 -----VADDRLLKICLCAEKYTCFVCGHVVAC 242
QY 593 QECAPSLRKPCICRGIIKGTVRTF 616
DB 243 GKCAAGVTTCPCVCRGQLDKAVRMV 266

RESULT 12
ID BIRE_MOUSE STANDARD; PRT; 1403 AA.
AC Q9R016; Q9R029; P81703; O09122; O09121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis inhibitory protein 5).
GN BIRC1E OR NAIP5 OR NAIP-RS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99431676; PubMed=10501978;
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct functional transcripts."
RN Mamm. Genome 10:1032-1035(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Sv;
RX MEDLINE=99417674; PubMed=10486205;
RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B., Kunkel L.M., Miller W., Dietrich W.F.;
RT "Comparative sequence analysis of the mouse and human Lgn1/SMART interval."
RN Genomics 60:137-151(1999).
RN [3]
RP SEQUENCE OF 82-168 FROM N.A.
RX STRAIN=129/Sv;
RX MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H., Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies within the Lgn1 critical interval and contains multiple copies of Naip exon 5."
RN Genomics 38:405-417(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF

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CC SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF135492; AAD56764.1; -
DR EMBL: AF131205; AAD56760.1; -
DR EMBL: U66326; AAC52974.1; -
DR HSSP: Q13490; IOBH.
DR MGD: MGI:1298220; Birc1e.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR_3.
DR SMART: SM00238; BIR_3.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50837; NACHT; 1.
DR Apoptosis; Repeat; Multigene family.
KW REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
FT CONFLICT 92 92 K -> R (IN REF. 1).
FT CONFLICT 144 144 S -> R (IN REF. 1).
FT CONFLICT 242 242 S -> G (IN REF. 2).
FT CONFLICT 472 472 T -> A (IN REF. 2).
FT CONFLICT 516 516 A -> D (IN REF. 2).
FT CONFLICT 521 521 A -> T (IN REF. 2).
FT CONFLICT 533 533 V -> A (IN REF. 2).
FT CONFLICT 538 538 S -> I (IN REF. 2).
FT CONFLICT 1092 1092 E -> D (IN REF. 2).
FT CONFLICT 1129 1129 H -> L (IN REF. 2).
FT CONFLICT 1137 1137 R -> Q (IN REF. 2).
FT CONFLICT 1242 1242 V -> I (IN REF. 2).
FT CONFLICT 1276 1276 D -> N (IN REF. 2).
SQ SEQUENCE 1403 AA; 159695 MW; B27F645043BCED42 CRC64;

Query Match 15.4%; Score 506; DB 1; Length 1403;
Best Local Similarity 27.3%; Pred. NO. 1.4e-25;
Matches 175; Conservative 73; Mismatches 216; Indels 176; Gaps 27;

QY 14 SYQNIKSTWEDSTILSDMTNSKQMKYDFSC-----LYRMSTYSTEPAGVPSERS 66
D 31 AFQVAKSQDEEE-----HKEMKMKKGFNSQMRSEAKRLKTFEYIDTRSWTP---QE 80
QY 67 LARAGFYTVGVNDKVKCFCCGIMLDNWKLGDSPIOKHKLQYFSCSFIONLVASISGTSK 126
D 81 MAAAGFYHTGVKLGVCQCCSLFLFNSLRKLPITERHKKLRPECEFLQ---GKDVGNIGK 137
QY 127 NTSPMRNSPAHSLSPTLEHSSLSFGSSYSSLPNPLNSRAVEDISSRTNPSYAMSTEEA 186
D 138 YDIRVK-----SPEKM-----LRGKARY--HEEEA 161
QY 187 RFLTYHMPPLTF--LSBSELARAGFYIIGPDVACFACGSKLSWPKDDAMSEHRRHF 244
D 162 RLSEFEDWPFYAGTSPVLSAAGFVTGKRDTVQCFSCGSGSYGNWEEGDDPWKEHAKMF 221
QY 245 PNCDFLEN--SLETLRSISNLSMOTHA-----R 272
D 222 PKCFELQSKSSSEIEAYIQSYEGFVHTGEHFKSWVRRELPMWSAYCNDVSFANEELR 281
QY 273 MRPEMYWSSVPOPEOLASAGFYVYGRNDVVKCFCCDGLRCWESGDDPWVEHAKMFP 332
D 282 MDMEKDMFOESPVEALVRAGFFYTKKDIYRCFCGCGCLEKMWEGDDPMEDHIKFFPE 341
QY 333 CEFLIRMGQ-EFVDEIGRYPHLLBOLSTSDTGEEN-ADFPITH----- 377
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D 342 CVFLQTLKSSAEVIPTLQSQY-----ALPEATEETRESNHDAAVHSTVVDLGSEAOV 396
QY 378 FGPESSSEDA-----VMNTPYVKSAL-----EMGFNBDLVKQTVQSKILTP 420
D 397 FOEARSLSBQLRNTYKATFRHNLNLPVCSSIGTDHLSCDYSIIKHSIQPVQ-EALTI 455
QY 421 GENKYTVDIVSALINADEKREEEK---EKOAEWASDDSLIRKRMALFOOLTVCVLP 477
D 456 PEVFSNLSVMC---VEGETSGKTYTFLKRIAFLWASGCCPLTYRPQLVFLYLSISITP 511
QY 478 ILDLULKANVINQOEHDIIKQTOIPLQARELIDTLVKGNAANFNKNC-KEIDSTLY 536
D 512 --DQGL-ANICAO-----LLGAGGCISEV---CLASSIQQLOLH 544
QY 537 KNLFVDKMKKIYPTEDVSG-L-SLEQLRRLQEE---RTC 571
D 545 QVLEFL-----LDYSGLASLPQALHTLTITKNTLSRTC 576

RESULT 13
BIR_MOUSE
ID BIR_MOUSE STANDARD; PRT; 1403 AA.
AC Q9JIB6; P81704; O09122; O09121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1f (Neuronal apoptosis
DE inhibitory protein 6).
GN BIRC1F OR NAIP6 OR NAIP-RS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid-10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
RA Endritzl M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array."
RL Genome Res. 10:1095-1102(2000).
RN [2]
RP SEQUENCE OF 82-168 FROM N.A.
RX STRAIN=129/SVJ;
RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
RT within the Lgnt critical interval and contains multiple copies of Naip
RT exon 5."
RL Genomics 38:405-417(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF242431; AAF82751.1; -
DR EMBL: U66327; AAC52975.1; -
DR HSSP: Q13490; IOBH.
DR MGD: MGI:1298222; Birc1f.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR_3.
DR SMART: SM00238; BIR_3.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
```


Db 525 -----GAGGCISEVCSSSIQQLQHVLF-----LDDYSG 556
QY 557 -SLEQLRLQEE---RTC 571
Db 557 ASLPALHTLTITKNYLFRTC 576

RESULT 15

IDL DROME STANDARD; PRT; 438 AA.

AC 024306; Q24306; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Apoptosis 1 inhibitor (inhibitor of apoptosis 1) (DIAP1) (Thread protein)

DE DIAP1 OR TH.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OC NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Eye Imaginal disk;

RX MEDLINE=96128128; PubMed=8548811;

RA Hay B.A., Massarman D.A., Rubin G.M.;

RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins

RT function to block cell death.";

RL Cell 83:1253-1262(1995).

CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND

CC HID-DEPENDENT CELL DEATH IN THE EYE.

CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.

CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC -----

DR EMBL: LA9440; AAC41609.1; .

DR HSSP: Q13490; IQBH.

DR Flybase: FBgn0003691; th.

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001841; Znf_fing.

DR Pfam: PF00097; zf-C3HC4; 1.

DR Pfam: PF00653; BIR; 2.

DR SMART: SM00238; BIR; 2.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS01282; BIR_REPEAT_1; 2.

DR PROSITE: PS50143; BIR_REPEAT_2; 2.

DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.

DR PROSITE: PS50089; ZF_RING_2; 1.

KM Apoptosis; Zinc-finger; Repeat.

FT REPEAT 44 110 BIR 1.

FT REPEAT 226 293 BIR 2.

FT ZN_FING 391 426 RING-TYPE.

SQ SEQUENCE 438 AA; 48098 MW; A6C22C8EDF5AEF29 CRC64;

Query Match 14.8%; Score 484; DB 1; Length 438;

Best Local Similarity 22.6%; Pred. No. 8e-25;

Matches 126; Conservative 62; Mismatches 128; Indels 242; Gaps 12;

QY 162 NSRAVE---DISSRRNPYSYASTEAREFLTYHMPLEFLSPSELARAGFYVIGPGR 217

Db 22 NTAATQLTKNNINKTRND---LNRETRLKTFTDPLDMLDKROLAQGTGFTTHAGDK 77

QY 218 VACFACGGKLSNWEKDDAMSEHRHFPNCP-----LENSLETLRFST- 261

Db 218 VACFACGGKLSNWEKDDAMSEHRHFPNCP-----LENSLETLRFST- 261

Db 78 VKCFECGVEIGCWEDQDPVPEHQWSPNCPLLRRRTNNVPINAEALDRILPPISTYD 137

QY 262 ----SNLSMOTHA----- 270

Db 138 GANDSTLEMRHAYAEVYIPMSQLIOSIGNMNAVNAAGSVTGTAPQPRVTATASTAQ 197

QY 271 -----ARMRTMYWSPSSVPVQPEQIASAGFYVGR 300

Db 198 ATGDVQPEFCRPSAASGNYPQYPEYAIETARLRFPEAMPNRLKQPHQLAEAGFYTCV 257

QY 301 NDDVYKFCDDGILRCWESDDPWEHAKWFPKCEFLIRMGQEEVDEIOGRYPILLEQL 360

Db 258 GDRVRCFCSCGGGLMDWMDNDEWEQHALWLSQCRFYKLMGQLYIDTVAK-PYLAEEKE 316

QY 361 STSDTGEENADPPIIHFGPGESSSDAVVMNTPVYKSALEMGNLDVKTVOISKILFT 420

Db 317 ESTSIGD-----TVAS----- 328

QY 421 GENYKTVNDIVSALLNMEDEKREKEKQAEEMASDLSLRKNMALFOQLTCVLPILD 480

Db 329 -----TQASEEQQTSLSSEAVSGDVA-----PSVAP--- 356

QY 481 NLKANVINKQEHDIKOKTQIPLOARELIDITLVKGNMAANIFKNCLEIDSTLYKNLF 540

Db 357 -----TAATRIFF-----NKI 366

QY 541 VDRNMKYIPTEDVSGLSLEQLRLRQERTCKVCMDEKVSVFIPCGHLVVCQCAPSLR 600

Db 367 VEATVATPSTNSSGST-----SIBEKLCIKICGAEYNTAFPLCGHYVACACASSVT 420

QY 601 KCPICRGIIKGVRTFLS 618

Db 421 KCPICRKPFPTDVMRVFS 438

Search completed: May 5, 2003, 16:02:40
Job time : 28.6313 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:57:12 ; Search time 150.94 Seconds

(without alignments)
843.627 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277

Sequence: 1 MHKTASQRLPFGPSYQNIKS.....LRKPCICGIIKGTVPFLS 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2630	80.3	589	11	Q9QZC6
2	2625	80.1	589	11	Q9ESE8
3	2339	71.4	610	13	Q57319
4	2185	66.7	602	11	Q9ESE9
5	1833	55.9	628	13	Q8UWD2
6	1318	40.2	374	11	Q921N0
7	1138.5	34.7	324	13	Q9DDN2
8	945.5	28.9	224	11	Q88642
9	898.5	27.4	501	11	Q9EQ05
10	898.5	27.4	501	11	Q9EQ04
11	896.5	27.4	496	11	Q9ESF0
12	894	27.3	493	13	Q8UVF8
13	801.5	24.5	197	13	Q91A69
14	796.5	24.3	195	13	Q91A70
15	737.5	22.5	498	5	Q960U3
16	684.5	20.9	405	13	Q8UWH2

17	500.5	15.3	346	5	Q968T8
18	494	15.1	597	11	Q9R015
19	490	15.0	438	5	Q9VUX5
20	486	14.8	281	12	Q9YNL8
21	481.5	14.7	379	5	Q9U492
22	479	14.6	403	5	Q8WPD9
23	476	14.5	264	12	Q9EN27
24	475.5	14.5	276	12	Q89744
25	470	14.3	261	12	Q9QES9
26	466.5	14.2	377	5	Q9N207
27	463.5	14.1	298	4	Q96CA5
28	462.5	14.1	280	4	Q9HAP7
29	460.5	14.1	236	4	Q96RW5
30	460.5	14.1	298	4	Q9H2A8
31	459.5	14.0	236	6	Q95W71
32	458.5	14.0	236	4	Q96EP9
33	457.5	14.0	236	6	Q95W72
34	456.5	13.9	402	5	Q8T621
35	423.5	12.9	313	12	Q9J827
36	396.5	12.1	276	12	Q80L95
37	368.5	11.2	268	12	Q91FT8
38	363.5	11.1	268	12	Q9E232
39	240	7.3	292	12	Q92394
40	239.5	7.3	210	4	Q9BQV0
41	231.5	7.1	284	12	Q9YKL5
42	222	6.8	285	12	Q9PYQ9
43	220	6.7	301	12	Q9P254
44	217.5	6.6	243	12	Q91EW1
45	207.5	6.3	517	11	Q8R4U8

ALIGNMENTS

RESULT 1
ID Q9QZC6 PRELIMINARY; PRT; 589 AA.
AC Q9QZC6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Dong Z., Denton M., Gu S.M., Salkumar P., Venkatachalam M.A.;
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF190020; AAF04585.1; -
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 589 AA; 66777 MW; E6812FEE3EA34142 CRC64;
Query Match 80.3%; Score 2630; DB 11; Length 589;
Best Local Similarity 81.7%; Pred. No. 1,6e-177;
Matches 488; Conservative 53; Mismatches 48; Indels 8; Gaps 4;

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QY 22 MEDSTILSDMTNSKOKAKKYDFSCELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKV 81
DB 1 MENSIVLSMTKKEKKKKYDFSCELYRMSTYSAFPRGVPVSESLARAGFYTTGVNDKV 60
QY 82 KCFCGGLMDNMKLGDSPIQKHQOLYRPSCSFTIONLVASLGSTSKNTSPMNSFAHSLSP 141
DB 61 KCFCGGLMDNMKLGDSPIQKHQOLYRPSCSFTIONLVASLGSTSKNTSPMNSFAHSLSP 118
QY 142 TLEHSLFSGSYSLSPNPLNSRAVEDISSRTPNPSYAMSTEAREFLTYHMPPLFLSP 201
DB 119 PLEQ---GGHSSLPSNPLNSRAVEDF-SLRNPPCSYAMSTEAREFLTYHMPPLFLSP 173
QY 202 SELARAGFYITGPDRAVACFACGKLSMWEPKDDAMSEHRRHPNCPFLNLSLETIRFSI 261
DB 174 AELAKAGFYITGPDRAVACFACGKLSMWEPKDDAMSEHRRHPNCPFLNLSLETIRFSI 233
QY 262 SNLSMOTHAARMRTFMYPSSVVPQEPOLASAGFYVGRNDVKCFCCDGLRCWESGDD 321
DB 234 SNLSMOTHAARMRTFMYPSSVVPQEPOLASAGFYVGRNDVKCFCCDGLRCWESGDD 293
QY 322 PVWEHAKWPPRCEFLIRMGQEFVDEIOGRYPHLLLEQLSTSDTTEENADPPIIHFGPG 381
DB 294 PVWEHAKWPPRCEFLIRMGQEFVDEIOGRYPHLLLEQLSTSDTTEENADPPIIHFGPG 353
QY 382 ESSSDAVAMNTPVYKSALEMGNRDLYQOTVOSKILTTGNYKYNDIVSALLNADEK 441
DB 354 E-NMEDAVAMNTPVYKSALEMGNRDLYQOTVOSKILTTGNYKYNDIVSALLNADEK 412
QY 442 REEKEKQAEEMASDDLSLIRKNRMALFQOLTQVPLDNLKANYINKQEHDIKOKTO 501
DB 413 REEKEKQAEEMASDDLSLIRKNRMALFQOLTQVPLDNLKANYINKQEHDIKOKTO 472
QY 502 IPLQARELIDTILYKGNAAANIFKNCLEIDSTLYKNLFVDKNMKYIPTEDVSGISLEEQ 561
DB 473 IPLQARELIDTILYKGNAAANIFKNCLEIDSTLYKNLFVDKNMKYIPTEDVSGISLEEQ 532
QY 562 LRRLOEERTCKVCMDEKSVFIPCGHLVWCECAPSLRKCPIRCGIKGVRTFLS 618
DB 533 LRRLOEERTCKVCMDEKSVFIPCGHLVWCECAPSLRKCPIRCGIKGVRTFLS 589

RESULT 2
Q9ESE8 PRELIMINARY: PRT: 589 AA.
AC Q9ESE8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holick M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes.";
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183431; AAG22971.1;
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HCA; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.

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DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD/CD285B CRC64;

Query Match      80.1%; Score 2625; DB 11; Length 589;
Best Local Similarity 81.6%; Pred. No. 3.7e-177;
Matches 487; Conservative 54; Mismatches 48; Indels 8; Gaps 4;

QY 22 MEDSTILSDMTNSKOKAKKYDFSCELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKV 81
DB 1 MENSIVLSMTKKEKKKKYDFSCELYRMSTYSAFPRGVPVSESLARAGFYTTGVNDKV 60
QY 82 KCFCGGLMDNMKLGDSPIQKHQOLYRPSCSFTIONLVASLGSTSKNTSPMNSFAHSLSP 141
DB 61 KCFCGGLMDNMKLGDSPIQKHQOLYRPSCSFTIONLVASLGSTSKNTSPMNSFAHSLSP 118
QY 142 TLEHSLFSGSYSLSPNPLNSRAVEDISSRTPNPSYAMSTEAREFLTYHMPPLFLSP 201
DB 119 PLEQ---GGHSSLPSNPLNSRAVEDF-SLRNPPCSYAMSTEAREFLTYHMPPLFLSP 173
QY 202 SELARAGFYITGPDRAVACFACGKLSMWEPKDDAMSEHRRHPNCPFLNLSLETIRFSI 261
DB 174 AELAKAGFYITGPDRAVACFACGKLSMWEPKDDAMSEHRRHPNCPFLNLSLETIRFSI 233
QY 262 SNLSMOTHAARMRTFMYPSSVVPQEPOLASAGFYVGRNDVKCFCCDGLRCWESGDD 321
DB 234 SNLSMOTHAARMRTFMYPSSVVPQEPOLASAGFYVGRNDVKCFCCDGLRCWESGDD 293
QY 322 PVWEHAKWPPRCEFLIRMGQEFVDEIOGRYPHLLLEQLSTSDTTEENADPPIIHFGPG 381
DB 294 PVWEHAKWPPRCEFLIRMGQEFVDEIOGRYPHLLLEQLSTSDTTEENADPPIIHFGPG 353
QY 382 ESSSDAVAMNTPVYKSALEMGNRDLYQOTVOSKILTTGNYKYNDIVSALLNADEK 441
DB 354 E-NMEDAVAMNTPVYKSALEMGNRDLYQOTVOSKILTTGNYKYNDIVSALLNADEK 412
QY 442 REEKEKQAEEMASDDLSLIRKNRMALFQOLTQVPLDNLKANYINKQEHDIKOKTO 501
DB 413 REEKEKQAEEMASDDLSLIRKNRMALFQOLTQVPLDNLKANYINKQEHDIKOKTO 472
QY 502 IPLQARELIDTILYKGNAAANIFKNCLEIDSTLYKNLFVDKNMKYIPTEDVSGISLEEQ 561
DB 473 IPLQARELIDTILYKGNAAANIFKNCLEIDSTLYKNLFVDKNMKYIPTEDVSGISLEEQ 532
QY 562 LRRLOEERTCKVCMDEKSVFIPCGHLVWCECAPSLRKCPIRCGIKGVRTFLS 618
DB 533 LRRLOEERTCKVCMDEKSVFIPCGHLVWCECAPSLRKCPIRCGIKGVRTFLS 589

RESULT 3
O57319 PRELIMINARY: PRT: 610 AA.
AC O57319;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE Inhibitor of apoptosis PROTEIN 1 (IAP) (Inhibitor of T cell apoptosis
DE PROMELINE).
GN IAP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-WHITE LEHORN; TISSUE=EMBRYONIC FIBROBLAST;
RX MEDLINE=98038801; PubMed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
RT mediator of the antiapoptotic activity of the v-Rel oncoprotein.";
RL Mol. Cell. Biol. 17:7328-7341(1997).

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CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CC CELLS.
CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
CC THE V-REL-TRANSFORMED CELLS.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
CC SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
CC IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC PROCESS.
CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
CC APOPTOSIS PROTEIN REPEAT).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL: AF008592; AAB8044.1; -.
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR Apoptosis; Zinc-finger; Repeat.
FT REPEAT 30 97 BIR_REPEAT 1.
FT REPEAT 176 242 BIR_REPEAT 2.
FT REPEAT 262 329 BIR_REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B4A6 CRC64;

Query Match 71.4%; Score 2339; DB 13; Length 610;
Best local Similarity 71.4%; Pred. No. 6, 1e-157;
Matches 437; Conservative 78; Mismatches 81; Indels 16; Gaps 7;

QY 20 SIMEDSTILSDWTNSNKQ--KMKYDFSCELYRMSTYSTEPAGVPSERSLARAGFYTG 77
DB 2 NIMDSPLASVVKONAHGELKYDLSCELYRMSTYSTEPAGVPSERSLARAGFYTG 61
QY 78 NDKVCFCCGMLDNWKLGDSPLOKHQOLYPSCSFIQNLVSA-SLG-ST-----SKN 127
DB 62 QDKVCFCCGMLDNWKLGDSPLOKHQOLYPSCSFIQNLVSA-SLG-ST-----SKN 121
QY 128 TSPMNSFAHSLSPLEHSSLSFGSYSSLPNPLNSRAVEDISSRTNPYSAMSTEAR 187
DB 122 LSPSLRSM--TLSPSEFGYGFSSFSFPDPTTRAEDI:SHLRKLNHNSMSTEAR 179
QY 188 FLYHMPPLFLSPSELARAGFYIGPGDRVACFACGKLSNWEPKDDAMSEHRRHPNC 247
DB 180 LRTFAMPLFLSPSELARAGFYIGPGDRVACFACGKLSNWEPKDDAMSEHRRHPNC 239
QY 248 PFLNSL-ETLRFISLNSMOTHAARMFTWVPSSVPOPEOLASAGFYVGRNDVYC 306
DB 240 PFVNLMDROPSEFVNSVNTMOTHEARVKTFINMPTRIPOPEOLASAGFYVGRNDVYC 299
QY 307 FCCGGGLRCWESGDDPWVEHAKWPRCEFLIRMGQEVDEIQGRYPHLLLEQLSTDT 366
DB 300 FCCGGGLRCWESGDDPWVEHAKWPRCEFLIRMGQEVDEIQGRYPHLLLEQLSTDT 359
QY 367 GEENADPPIHFGESSESDAVAMNTPVVKSALEMGFNRDLVKQTVQSKILLTGENYKT 426
DB 360 VDEEND-PIHFEGESSESDAIVMNTPVKALLEMGFNRDLVKQTVQSKILLTGENYKT 418
QY 427 VNDIYALNAEDEKREKEKEKAEEMASDDLSLRKNRMALFQQLTCVPLTDLNLLKAN 486
DB 419 VNDIYALNAEDEKREKEKEKAEEMASDDLSLRKNRMALFQQLTCVPLTDLNLLKAN 478
QY 487 VINKOEHDIKQKQIPIQARELIDTILYKNAANIFKNCLEISTLYNLNLFVDKMK 546
DB 487 VINKOEHDIKQKQIPIQARELIDTILYKNAANIFKNCLEISTLYNLNLFVDKMK 546
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DB 479 VITELEHDYIKQKTQPIQARELIDTILYKNAANIFKNCLEISTLYNLNLFVDKMK 538
QY 547 YIPEDVSGISLEQLRLQOEERTCKVMDKEVSVFIPCGHLVYCOECAPSLRKPICR 606
DB 539 YIPEDVSGISLEQLRLQOEERTCKVMDKEVSVFIPCGHLVYCOECAPSLRKPICR 598
QY 607 GIINKGTVPFELS 618
DB 599 GTIKGTVPFELS 610

RESULT 4
Q9ESE9 PRELIMINARY; PRT; 602 AA.
AC Q9ESE9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183430; AAC22970.1; -.
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR Apoptosis; Zinc-finger.
KW ZINC-FINGER.
SQ SEQUENCE 602 AA; 67326 MW; CC91385E6A62DE5A CRC64;

Query Match 66.7%; Score 2185; DB 11; Length 602;
Best local Similarity 67.4%; Pred. No. 4, 5e-146;
Matches 411; Conservative 86; Mismatches 93; Indels 20; Gaps 7;

QY 20 SIMEDSTILSDWTNS-NKQMKYDFSCELYRMSTYSTEPAGVPSERSLARAGFYTG 78
DB 2 NMDQSAFLAKLMSADYFELKYDFSCELYRMSTYSTEPAGVPSERSLARAGFYTG 61
QY 79 DKVCFCCGMLDNWKLGDSPLOKHQOLYPSCSFIQNLVSA-----LGSTSKNTS 129
DB 62 DKVCFCCGMLDNWKLGDSPLOKHQOLYPSCSFIQNLVSA-----LGSTSKNTS 119
QY 130 PMRNSFAHSLSPLEHSSLSFGSYSSLPNPLNSRAVEDISSRTNPYSAMSTEAR 189
DB 120 TMSGFAAS-----ESTGFGSSYSFSDPVNFRANODCPAFSTSTYHFMNTEARLL 174
QY 190 TYHMPPLFLSPSELARAGFYIGPGDRVACFACGKLSNWEPKDDAMSEHRRHPNC 249
DB 175 TYQWPLFLSPSELARAGFYIGPGDRVACFACGKLSNWEPKDDAMSEHRRHPNC 234
QY 250 LENSEL-TLRFISLNSMOTHAARMFTWVPSSVPOPEOLASAGFYVGRNDVYC 308
DB 235 LKDVQFTSQYTVSNLSMOTHAARMFTWVPSSVPOPEOLASAGFYVGRNDVYC 294
QY 309 CDGGLRCWESGDDPWVEHAKWPRCEFLIRMGQEVDEIQGRYPHLLLEQLSTDTTGE 368
DB 309 CDGGLRCWESGDDPWVEHAKWPRCEFLIRMGQEVDEIQGRYPHLLLEQLSTDTTGE 368
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Db 295 CDGGLRCWESGDDPWEVHAKEWPCFCEYLIRIKGOEFVGVQAGYPHLLEQLLSTSDSPED 354
Qy 369 ENADPPIIHFGPGESESDAVMMNTPVYKSALEMGNRLVKTQVSKILITGENKTVN 428
Db 355 ETGEAIVHLGPGE-NMEDAVMMNTPVYKSAALDMGFSRLVKTQVSKILITGENKTVN 413
Qy 429 DIVSALLNMEDEKREKEKEQAEEMASDLSLRKNRAALFQOLTCVLPILNLLKANYI 488
Db 414 DLVIGLDADEMBREQTEQAESEESDLSLRKNRAALFQOLTCVLPILNLLKANYI 473
Qy 489 NKQEHDIKQKQIPLQARELIDTILVKGMAANIFKNCJKEIDSTLYKNLFVDKNMKYI 548
Db 474 TEQETDAVKQKPH-TLQARTLIDIVLAKNTAATSFRRSIQEIIDPGLYRDIIVRQNRSL 532
Qy 549 PTEDEVSGLSLEQLRLQERTCKVCMDEKVSVEIPCGHLVYQECAPSLRKCPICRGI 608
Db 533 PTDDIALPMEQLRLQERTCKVCMDEKVSVEIPCGHLVYQECAPSLRKCPICRGT 592
Qy 609 IKGTVRTFLS 618
Db 593 IKGTVRTFLS 602

RESULT 5
Q8UMD2 PRELIMINARY; PRT: 628 AA.
AC Q8UMD2;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Iap1.
GN Iap1.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."
RT Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF442500; AL33679.1; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR. 3.
DR Pfam: PF00619; CARD. 1.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00238; BIR. 3.
DR SMART: SM00114; CARD. 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 55.9%; Score 1833; DB 13; Length 628;
Best Local Similarity 56.1%; Pred. No. 3.5e-121;
Matches 353; Conservative 101; Mismatches 141; Indels 34; Gaps 9;
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Db 63 RVQCFRCNTADNMQSGDCPAERHKLSPNCSEFIQSLPATANLSSSHSAFSLRNVAVL 122
Qy 138 SLSE-----PTLHSSLSFGSYSLSP-NPLNSRAVEDISSRT----NP 176
Db 123 QLSAPATAAPSTAPSTSGQTEOVGYLNMGFTNLAPSSPISRGVDMHQRPACHPN 182
Qy 177 YSANSTEAREFLTYHMPDLTFLSPSELARAGFYIIGPDVYACFACGKLSNMEPKDA 236
Db 183 --GMRREERLDTFQNMWTLATVPAELAKAGLYLQGDVYACFSCGGQLSWEGRDRA 239
Qy 237 MSEHRRHFPNCPLE-NSLETFRS-----ISNLSMOTHAARMRTFMWSSVPQPEQ 289
Db 240 VSEHQRYHPCRFYGRDRADNIPLSGGGLSNVSNAMQCEERLLTFVNMPSRIIPYRPDQ 299
Qy 290 LASAGFYIYGRNDVYKFCDDGGLRCWESGDDPWEVHAKEWPCFCEYLIRIKGOEFYDEIQ 349
Db 300 LAKAGFYIYGRNDVYKFCDDGGLRCWESGDDPWEVHAKEWPCFCEYLIRIKGOEFYHQIQ 359
Qy 350 GRYPHLLEQLLSTDTGGEENADPPIIHFGPGESESDAVMMNTPVYKSALEMGNRLV 409
Db 360 ARFPLFEQLLTNGDSNSREFVDPVYHLGPGEDRSEDVAMANNPVYKSALEMGFERGLV 419
Qy 410 KQVOSKILITGENKTVNDIVSALLNMEDEKREKEKEQAEEMASDLSLRKNRAALF 469
Db 420 KQVOSKILITGENKTVQELVSDLSAEDKEKEEERELAEEMASDGFTEFLKHHAAIS 479
Qy 470 QQLTCVLPILNLLKANYINKQEHDIKQKQIPLQARELIDTILVKGMAANIFKNCJKE 529
Db 480 QRLKSVQSLMDHLEENVISQKEVDSIRNCTSVKQQTGQLIDLVLSKGNAAAEVFRNMIX 539
Qy 530 EIDSTLYKNLFVDKNMKYIPTEDVSGLSLEQLRLQERTCKVCMDEKVSVEIPCGHL 589
Db 540 KNDVYLRLEMAQNEAASPSQSDLPMEQLRLQERTCKVCMDEKVINIVFICGHL 599
Qy 590 VVQECAPSLRKCPICRGIIGKTVRTFLS 618
Db 600 VVQECAPSLRKCPICRGMVKGTVRTFLS 628

RESULT 6
Q921NO PRELIMINARY; PRT: 374 AA.
ID Q921NO;
AC Q921NO;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to baculoviral IAP repeat-containing 2.
GN BIRC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC011338; AAH11338.1; -
DR MGD: MGI:1197007; Birc2.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR. 3.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 40.2%; Score 1318; DB 11; Length 374;
Best Local Similarity 66.7%; Pred. No. 4.1e-85;
Matches 242; Conservative 49; Mismatches 54; Indels 18; Gaps 5;
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[illegible]

RESULT 7

ID	Q9DDN2	PRELIMINARY;	PRT;	324 AA.
AC	Q9DDN2;			
DT	01-MAR-2001 (TREMBlrel. 16, Created)			
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	Apoptosis inhibitor ch-IAP1 (Fragment).			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
CC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;			
RT	"The Apoptosis Inhibitor ch-IAP1 Is a Direct Transcriptional Target of			
RT	v-Rel and c-Rel.";			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF311289; AAG42316.1; -.			
DR	HSSP; Q13490; IOBH.			
DR	InterPro; IPR001370; BIR.			
DR	Pfam; PF00653; BIR; 3.			
DR	SMART; SM00238; BIR; 3.			
DR	PROSITE; PS01282; BIR_REPEAT_1; 1.			
DR	PROSITE; PS0143; BIR_REPEAT_2; 3.			
FT	NON_TER 324			
SO	SEQUENCE 324 AA; 36567 MW; 5E2B89DEAE3733F3 CRC64;			

Query Match	34.7%	Score 1138.5	DB 13	Length 324
Best Local Similarity	63.4%	Pred. No. 1.6e-72		
Matches 206; Conservative	49;	Mismatches 53;	Indels 15;	Gaps 6;

[illegible][illegible]

RESULT 8

088642			
ID	088642	PRELIMINARY;	PRT; 224 AA.
AC	088642;		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)		
DE	Inhibitor of apoptosis protein (fragment).		
GN	RIAP1.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=WISTAR; TISSUE=OVARY;		
RA	Bradley C.K.; Lareu R.R.; Dharmarajan A.M.;		
RT	"Cloning and characterisation of an inhibitor of apoptosis protein		
RT	(IAP) in the rat corpus luteum."		
RL	Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AF081503; AAC32497.1; -.		
DR	HSSP; Q13490; IQB8.		
DR	InterPro; IPR001370; BIR.		
DR	Pfam; PF00653; BIR; 3.		
DR	SMART; SM00238; BIR; 2.		
DR	PROSITE; PSS0143; BIR_REPEAT_2; 3.		
FT	NON_TER 1		
FT	NON_TER 1		
FT	NON_TER 224		
SEQUENCE	224 AA; 213A52534D5EB56A CRC64;		

Query Match	28.9%	Score 945.5	DB 11	Length 224
Best Local Similarity	74.9%	Pred. No. 4.2e-59		
Matches 133	Conservative	18	Mismatches 33	Indels 7
				Gaps 3

QY 93 WKAGDSPIQKHQOLYPCSCFIQNLVNASLGSRTSKNTSPMRNSAHSLSPTLEHSSLSGGS 152
 Db 1 WKQGDSPTEKHQOIFYPCSCFVQTLSSGGLQSAKNTSPAKSRRAHSL-PLRD-...-GGI 54
 QY 153 YSSLSPNPNSRAVEDISSSRNPYSIAMSTEBARFLTYHMAPLTFSSPSSELAAPAGFYI 212
 Db 55 HSSLPSNPNSRAVEDE-SLRNPNPCSYAMSTEBARFLSYSMNPLSFLSPALZGAKAIFYT 113
 QY 213 GPGDRVACFACGGKLSHWEPEPKDAMSEHRRHPNCPLENSLETLRFSISRTSKQTTAAR 272
 Db 114 GGQDRVACFACGGKLSHWEPEPKDAMSEHRRHPNCPLENSLETLRFSISRTSKQTTAAR 173
 QY 273 MRTFMWYSPVQPEQLASAGFYIYVRNDVDKCFCCDGGGLRCWESGDDPW 323
 Db 174 MTFLLYPPSSVLPQPEQLASAGFYIYVHNDVDKCFCCDGGGLRCWEPGDDPW 224

RESULT 9

ID	Q9EQ05	PRELIMINARY;	PRT;	501 AA.
AC	Q9EQ05;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
-DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Inhibitor of apoptosis protein 3.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
OX	NCBI_TaxID=10116;			

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-OVARY;
RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
   protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF304333; AAG41192.1;
DR HSSP; Q13490; 1QBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR Zinc-finger.
SQ SEQUENCE 501 AA; 56548 MW; 0973FBF28E81C5A0 CRC64;

Query Match          27.4%; Score 898.5; DB 11; Length 501;
Best Local Similarity 33.4%; Pred. No. 2.7e-55;
Matches 204; Conservative 84; Mismatches 150; Indels 173; Gaps 15;

OY 33 NSNKKMYDFSCELYRMSTYTFPAGVPVSRSLARAGFYTYGVNDKVCFCGCLMLDN 92
    16 DTNKEDE---EFVEEFNRLKTFANFPSSPVASSTLARAGFLYTGEDTVQCFSCHAAYDR 72
OY 93 WKLGDSPIQKHQKQLYPSCSFIONLVASLSGSTSKNTSP-----MRNSFAHS 138
    73 WQYGDASVGRHRRISPCRFINGFYFEN-GAT-QSTSPGIONGOYKSENCVGNRHFA-- 128
OY 139 LSPTEHSSLSFGSYSSLSPNLNSRAVEDISSRTPNPSYAMSTEAREFLTYHMP-LT 197
    129 ---LDRPSETHADYL-----LRTGVVDISDT-IYPRNPAMCESEARLKTQNPDPYA 177
OY 198 FLSPSELARAGFYTYIGDRAVACFACGKLSNWEPRKDDAMSEHRRHFPNCPFL----- 250
    178 HLSPRELASAGLYTYTGIDQVQCFCCGKLNWEPKDDRAMSEHRRHFPNCFVYGRNVN 237
OY 251 -----ENSLFTLRFSISNLSMOTHAARMRTFMYPSSVPVOPQOLASAGFYV 298
    238 RSESGVSSDRNFPNSTNSPR---NPMAEYDARIYTFGTWLYS--VNKEQLARAGFYAL 291
OY 299 GRNDVYKFCFCCDGLRCWESGDDPWVEHAKWFPCEFLIRKGOEFVDEIOGRYPHLEQ 358
    292 GEGDKVKCFHCGGGLADWKPSDDPWQHAHWPGCKYLLDEKGOEYINNI-----HLTHS 346
OY 359 LSTSDTTEGENADPPIIHFGPGESSSEDAVMNTPVKSALEMGFNRDLVKOTVQSKIL 418
    347 LGSVSVRTAEKT-----PSVTKKIDPTIFQNPVQEAIRMGFNFKDIKKTMEEKIQ 397
OY 419 TTGENTYTVNDIVSALLNAEDKREBEKEKQAEEMASDDLILIRKRMALFQOLTCLVPI 478
    398 TSGSNYLSLEVLIADIVSAQKDNODE-----424
OY 479 LDNLKANVINQOEHDIIKQTOIPLQARELIDTILYKGNAAANIFKNCLEIDSTLYKN 538
    425 -----SSQTSIQ-----431
OY 539 LFVDKNNKIYPTEDVSGLSLEQLRLQOEERTCKVCMDEKSVVFIIPGHLVYVCOECAPS 598
    432 -----KDISTEQLRLQOEKLCIKCMDRNIAIYFVPGCHLVYTKQCAEA 476
OY 599 LRKCPICRGII 609
    477 VDKCPACCTVI 487
DB

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AC Q9EQ04;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid-10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-OVARY;
RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
   protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF304334; AAG41193.1;
DR HSSP; Q13490; 1QBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR Zinc-finger.
SQ SEQUENCE 501 AA; 56578 MW; 4863F69FE2E0C8CD CRC64;

Query Match          27.4%; Score 898.5; DB 11; Length 501;
Best Local Similarity 33.4%; Pred. No. 2.7e-55;
Matches 204; Conservative 84; Mismatches 150; Indels 173; Gaps 15;

OY 33 NSNKKMYDFSCELYRMSTYTFPAGVPVSRSLARAGFYTYGVNDKVCFCGCLMLDN 92
    16 DTNKEDE---EFVEEFNRLKTFANFPSSPVASSTLARAGFLYTGEDTVQCFSCHAAYDR 72
OY 93 WKLGDSPIQKHQKQLYPSCSFIONLVASLSGSTSKNTSP-----MRNSFAHS 138
    73 WQYGDASVGRHRRISPCRFINGFYFEN-GAT-QSTSPGIONGOYKSENCVGNRHFA-- 128
OY 139 LSPTEHSSLSFGSYSSLSPNLNSRAVEDISSRTPNPSYAMSTEAREFLTYHMP-LT 197
    129 ---LDRPSETHADYL-----LRTGVVDISDT-IYPRNPAMCESEARLKTQNPDPYA 177
OY 198 FLSPSELARAGFYTYIGDRAVACFACGKLSNWEPRKDDAMSEHRRHFPNCPFL----- 250
    178 HLSPRELASAGLYTYTGIDQVQCFCCGKLNWEPKDDRAMSEHRRHFPNCFVYGRNVN 237
OY 251 -----ENSLFTLRFSISNLSMOTHAARMRTFMYPSSVPVOPQOLASAGFYV 298
    238 RSESGVSSDRNFPNSTNSPR---NPMAEYDARIYTFGTWLYS--VNKEQLARAGFYAL 291
OY 299 GRNDVYKFCFCCDGLRCWESGDDPWVEHAKWFPCEFLIRKGOEFVDEIOGRYPHLEQ 358
    292 GEGDKVKCFHCGGGLADWKPSDDPWQHAHWPGCKYLLDEKGOEYINNI-----HLTHS 346
OY 359 LSTSDTTEGENADPPIIHFGPGESSSEDAVMNTPVKSALEMGFNRDLVKOTVQSKIL 418
    347 LGSVSVRTAEKT-----PSVTKKIDPTIFQNPVQEAIRMGFNFKDIKKTMEEKIQ 397
OY 419 TTGENTYTVNDIVSALLNAEDKREBEKEKQAEEMASDDLILIRKRMALFQOLTCLVPI 478
    398 TSGSNYLSLEVLIADIVSAQKDNODE-----424
OY 479 LDNLKANVINQOEHDIIKQTOIPLQARELIDTILYKGNAAANIFKNCLEIDSTLYKN 538
    425 -----SSQTSIQ-----431
OY 539 LFVDKNNKIYPTEDVSGLSLEQLRLQOEERTCKVCMDEKSVVFIIPGHLVYVCOECAPS 598
    432 -----KDISTEQLRLQOEKLCIKCMDRNIAIYFVPGCHLVYTKQCAEA 476
DB

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QY 599 LRKPCIRGII 609
Db 477 VDKPMTCTVI 487

RESULT 11

Q9ESF0 PRELIMINARY; PRT; 496 AA.
AC Q9ESF0; 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF183429; AAC22969.1; -
DR HSP; Q13490; 10BH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; Zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
KW Zinc-finger.
SQ SEQUENCE 496 AA; 56117 MW; 98EF142AECB798 CRC64;

Query Match 27.4%; Score 896.5; DB 11; Length 496;
Best Local Similarity 33.1%; Pred. No. 3.6e-55;
Matches 205; Conservative 86; Mismatches 155; Indels 173; Gaps 15;

QY 33 NSNKKMKYDSCCLYRMSTYTPAGVYVSERSLARAGFYTGVDKVKCFCCGLMIDN 92
Db 16 DTNKE--EFVEEFRLKTFANFPSSPVASATLARAGELVTGEGDTVQCSCHAADVDR 72
QY 93 WKLGDSPIQKHQOLYPCSFIONLVASLSTSKNTSP-----MRNSFAHS 138
Db 73 WQYGDASVGRHRISNCRINGFYFEN-GAT-OSTSPICNGOYKSCNCGNRNHA-- 128
QY 139 LSPLEHSSLSFGSYSLSPNPLNSRAVEDISSRTNPYSYAMSTEAREFLTYHMP-LT 197
Db 129 ----LDRPSETHADYL-----LRTGVVDISDT-IYPRNPACSEEARPKTFQWBDYA 177
QY 198 FLSPSELARAGFYIIGPDVACFCAGKLSNMWPKDAMSEHRRHFPNCPFL----- 250
Db 178 HLSPRELASAGLYTGIDDOVQCFCGCKLKMWPCDRAWSSEHRRHFPNCFVLGRNVN 237
QY 251 -----ENSLTLRFSISLSMOTHAARMRTMYWSSVPVQPEOLASAGFYTV 298
Db 238 RSEGSVSSDRNFPNINSR-----NPAMAEYDARIVTGTWLYS--VAKEQLARAGYAL 291
QY 299 GRANDVKCFCCDGLRCWESGDDPVVEHAKWFPCEFLIRMGQEFVDEIGRYPHLEQ 358
Db 292 GEGDKKCFHCGGGLTDWKPSEDPEWQHAKWPGCKYLDKQGEYINNI-----HLTHS 346
QY 359 LLSTSTTGEENADPPIIHGPGSESSDAVMNTPYVKSALMGFNLDLVQTVOSKIL 418
Db 347 LGESVVRTAERT-----PSYVKKIDDTIFQNPVQEAIRMGFNFKDIDKTMEEKIQ 397
QY 419 TTGENKTVNDIVSALLNADEKREBEKEQAEMASDLSLIRKNRAALFOQLTCVLP 478
Db 398 TSGSNLISLEVLIALDVSQAKDNQD----- 424

QY 479 LDNLKANVINKQEHDIKQTOIPLQARELIDPILVKGNAANIFKNCLKKEIDSTLYKN 538
Db 425 -----SSQSTLQ----- 431

QY 539 LFVDKMKYIPTEVDYSGLSLEQRLRLQERTCKYCMKEVSVYFPCGHLVYCQECAPS 598
Db 432 -----KDISTEQLRLQEEKLCKICMORNIATVFPVCGHLVYCQCAEA 476

QY 599 LRKPCIRGIIKGVTFPL 617
Db 477 VDKPMTCTVITFKOKIFM 495

RESULT 12

Q8UVF8 PRELIMINARY; PRT; 493 AA.
AC Q8UVF8; 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP
RT (IAP3)."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF451854; AAL47170.1; -
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; Zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match 27.3%; Score 894; DB 13; Length 493;
Best Local Similarity 34.5%; Pred. No. 5.4e-55;
Matches 210; Conservative 77; Mismatches 150; Indels 172; Gaps 18;

QY 30 DNTSNKKMKYDFSCCLYRMSTYTPAGVYVSERSLARAGFYTGVDKVKCFCCGLM 89
Db 22 EWTQ-----EHYRLGTVEFPHDCPVASALARAGFYTGVDKVKCFSCGHT 69
QY 90 LDNWKLGDSPIQKHQOLYPCSFIONLVASLSTSKNTSPMNSFAH-----SLS 140
Db 70 VEGWEPGDSADIRHKNLSPDCRFITG--SAFL--ENNVPVLOVSHORTENGSSNLALP 124
QY 141 PLEHSSLSFGSYSLSPNPLNSRAVEDISSRTNPYSYAMSTEAREFLTYHMP-PLTF 199
Db 125 SALEDLSVDEADYL-----LRTGVVMDSDT-LYKPNPACSEEARLKSFNHWPPYGL 177
QY 200 SPEELARAGFYIIGPDVACFCAGKLSNMWPKDAMSEHRRHFPNCPFL-----ENS 253
Db 178 TPKELASAGLYTGVDAVACFCGCKLKMWPCDRAWSSEHRRHFPNCFVLAGRDVGNVS 237
QY 254 LETLRFSI-----NLSTQTHAARMRTMYWSSVPVQPEOLASAGFYTVGRND 302
Db 238 TDSICAEIAGRSCLNNEQHPRNPMSAEYERRIQTFLLW--IYVKNKEHLAAGFYSTGND 295
QY 303 DYKCFCCDGLRCWESGDDPVVEHAKWFPCEFLIRMGQEFVDEIGRYPHLEQLIST 362
Db 296 HVCFFHCGGLQEWENEDBDWQAKWPGCKFLRDEKLEFINTNV-----HLRD--GC 347

[illegible]

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RESULT 13
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ID 09IA69 PRELIMINARY; PRT; 197 AA.
AC 09IA69:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauiria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
SEQUENCE FROM N.A.
RR STRAIN-BREED FAYOUMI; TISSUE=SPLEEN;
RC MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
RT specific genes.";
RL Poult. Sci. 80:284-288(2001).
DR EMBL; AF221083; AAF35320.1; -.
DR HSSP; Q13490; IQBH.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 197
SEQUENCE 197 AA; 22602 MW; D79232DABCF623E1A CRC64;

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[illegible]

ID	Q91A70	PRELIMINARY;	PRT;	195 AA.
AC	Q91A70;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)			
DE	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE	Inhibitor of apoptosis 1 (Fragment).			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
NC	NCBI_taxid=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BREED LEHORN; TISSUE-SPLEEN;			
RX	MEDLINE=21158006; PubMed=11261557;			
RA	Zhou H., Liu W., Lamont S.J.;			
RT	"Genetic variation among chicken lines and mammalian species in			
RT	specific genes.";			
RL	Poult. Sci. 80:284-288(2001).			
DR	EMBL; AF221082; AAF35319.1; .			
DR	HSSP; Q13490; 10BH.			
DR	InterPro; IPR001370; BIR.			
DR	Pfam; PF00653; BIR; 2.			
DR	SMART; SM00238; BIR; 2.			
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.			
DR	PROSITE; PS50143; BIR_REPEAT_2; 2.			
FT	NON_TER	1		
FT	NON_TER	1		
SQ	SEQUENCE	195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;		
Query Match	24.3%;	Score 796.5;	DB 13;	Length 195;
Best Local Similarity	68.2%;	Pred. No. 1.2e-48;		
Matches 133;	Conservative 33;	Mismatches 28;	Indels 1;	Gaps 1;
QY	155 SLSPNPENLSRAVEDISSRTNPYSYAMSTEARFLTYMMWPLTFLSPSELARAGFYITGP	214		
DB	1 SFQDPVYTRRAEDLSLRKSLKLNPSMSTEARLRTFHAMPLMFLSPAELAKAGLYYIGT	60		
QY	215 GDRVACFACAGKSLNWEPRKDDAMSEHRRHFPNCPFLENSL-ETLRFSLNLSMOTHAAM	273		
DB	61 ADVACFCFCGGLSNWEPRKDNAMSEHRRHFPNCPFVENLMRDGSPFVNSVNTWQTHEARV	120		
QY	274 RTFMWPSVPVPOEOLASAGFYVGRNDVYKFCFCCDGLRCWESGDDPWVEHAKWPRC	333		
DB	121 KTIINWPTRIIPVPOEOLADAGFYVGRNDVYKFCFCCDGLRCWESGDDPWIEHAKWPRC	180		
QY	334 EFLIRMGQEFVDEI	348		
DB	181 EYLRVKGGEFVSQV	195		

RESULT	15	
Q960U3		
ID	Q960U3	PRELIMINARY; PRT; 498 AA.
AC	Q960U3;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE	LB34777P.	
GN	IAP2 OR CG8293.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BERKELEY;	
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,	

May 6 18:23:48 2003

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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 3.73848 Seconds

(without alignments)
432.866 Million cell updates/secTitle: US-08-569-749-5
Perfect score: 307
Sequence: 1 CELYRMSTYSTFPAGVPVSE.....KVKCFCCGLMDNWKLGDSP 55Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summariesDatabase : Issued_Patents_AA:*
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2: /cgcn2_6/ptodata/1/1aa/5B.COMB.rep:*
3: /cgcn2_6/ptodata/1/1aa/6A.COMB.rep:*
4: /cgcn2_6/ptodata/1/1aa/6B.COMB.rep:*
5: /cgcn2_6/ptodata/1/1aa/PCFUS.COMB.rep:*
6: /cgcn2_6/ptodata/1/1aa/backfiles1.rep:*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	55	4	US-08-569-749-5
2	307	100.0	55	5	PCT-US96-12860-5
3	307	100.0	618	2	US-08-511-485-8
4	307	100.0	618	3	US-09-212-971-8
5	307	100.0	618	4	US-08-800-929A-8
6	307	100.0	618	4	US-08-569-749-2
7	307	100.0	618	4	US-09-617-053A-8
8	307	100.0	618	4	US-09-069-023-29
9	307	100.0	618	5	PCT-US96-12860-2
10	301	98.0	55	4	US-08-569-749-6
11	301	98.0	55	5	PCT-US96-12860-6
12	301	98.0	604	2	US-08-511-485-6
13	301	98.0	604	3	US-09-212-971-6
14	301	98.0	604	4	US-08-800-929A-6
15	301	98.0	604	4	US-08-569-749-4
16	301	98.0	604	4	US-09-617-053A-6
17	301	98.0	604	5	PCT-US96-12860-4
18	298	97.1	68	2	US-08-511-485-19
19	292	95.1	68	2	US-08-511-485-18
20	291	94.8	612	3	US-09-212-971-14
21	291	94.8	612	4	US-08-800-929A-14
22	291	94.8	612	4	US-08-569-749-14
23	291	94.8	612	4	US-09-617-053A-14
24	291	94.8	612	5	PCT-US96-12860-14
25	284	92.5	600	3	US-09-212-971-12
26	284	92.5	600	4	US-08-800-929A-12
27	284	92.5	600	4	US-09-617-053A-12

28	159	51.8	68	2	US-08-511-485-17	Sequence 17, Appl
29	159	51.8	497	2	US-08-511-485-4	Sequence 4, Appl
30	159	51.8	497	3	US-09-212-971-4	Sequence 4, Appl
31	159	51.8	497	4	US-08-800-929A-4	Sequence 4, Appl
32	159	51.8	497	4	US-09-617-053A-4	Sequence 4, Appl
33	153	49.8	68	2	US-08-511-485-16	Sequence 16, Appl
34	153	49.8	496	2	US-08-511-485-10	Sequence 10, Appl
35	153	49.8	496	3	US-09-212-971-10	Sequence 10, Appl
36	153	49.8	496	4	US-08-800-929A-10	Sequence 10, Appl
37	153	49.8	496	4	US-09-617-053A-10	Sequence 10, Appl
38	150	48.9	438	5	PCT-US95-05922A-2	Sequence 2, Appl
39	138	45.0	68	2	US-08-511-485-27	Sequence 27, Appl
40	133	43.3	68	2	US-08-511-485-26	Sequence 26, Appl
41	132	43.0	68	2	US-08-511-485-28	Sequence 28, Appl
42	132	43.0	268	3	US-08-836-134-22	Sequence 22, Appl
43	132	43.0	268	4	US-09-493-784-22	Sequence 22, Appl
44	130	42.3	68	2	US-08-511-485-21	Sequence 21, Appl
45	128	41.7	68	2	US-08-511-485-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-569-749-5
Sequence 5, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-5

Query Match 100.0%; Score 307; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 4.9e-37;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDVKKCFCCGLMDNWKLGDSP 55
DB 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDVKKCFCCGLMDNWKLGDSP 55

RESULT 2
PCT-US96-12860-5
Sequence 5, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBERTSON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Breznet, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-5

Query Match 100.0%; Score 307; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 4.9e-37;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 55
DB 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 55

RESULT 3
US-08-511-485-8
Sequence 8, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-8

Query Match 100.0%; Score 307; DB 2; Length 618;
Best Local Similarity 100.0%; Pred. No. 9.1e-36;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 99

RESULT 4
US-09-212-971-8
Sequence 8, Application US/092129718
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-8

Query Match 100.0%; Score 307; DB 3; Length 618;
Best Local Similarity 100.0%; Pred. No. 9.1e-36;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 99

RESULT 5
US-08-800-929A-8

Sequence 8, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-8

Query Match 100.0%; Score 307; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 9.1e-36;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKYKCFCCGMLDNWKLGDSP 55
Db 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKYKCFCCGMLDNWKLGDSP 99

RESULT 6
US-08-569-749-2
Sequence 2, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-2

Query Match 100.0%; Score 307; DB 4; Length 618.
Best Local Similarity 100.0%; Pred. No. 9.1e-36;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKYKCFCCGMLDNWKLGDSP 55
Db 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKYKCFCCGMLDNWKLGDSP 99

RESULT 7
US-09-617-053A-8
Sequence 8, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-617-053A-8

Query Match 100.0%; Score 307; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 9.1e-36;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKYKCFCCGMLDNWKLGDSP 55
Db 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKYKCFCCGMLDNWKLGDSP 99

RESULT 8

US-09-069-023-29
; Sequence 29, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 29
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-29

Query Match 100.0%; Score 307; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 9.1e-36;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKCFCCGMLDNNKLGSP 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKCFCCGMLDNNKLGSP 99

RESULT 9

PCT-US96-12860-2
; Sequence 2, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-12860-2

Query Match 100.0%; Score 307; DB 5; Length 618;

Best Local Similarity 100.0%; Pred. No. 9.1e-36;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKCFCCGMLDNNKLGSP 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKCFCCGMLDNNKLGSP 99

RESULT 10

US-08-569-749-6
; Sequence 6, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Goeddel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,749
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-749-6

Query Match 98.0%; Score 301; DB 4; Length 55;
Best Local Similarity 98.2%; Pred. No. 3.6e-36;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKCFCCGMLDNNKLGSP 55
DB 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVKCFCCGMLDNNKLGSP 55

RESULT 11

PCT-US96-12860-6
; Sequence 6, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-6

Query Match 98.0%; Score 301; DB 5; Length 55;
Best Local Similarity 98.2%; Pred. No. 3.6e-36;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVKCFCCGMLDNKRLGDS 55
DB 1 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVKCFCCGMLDNKRLGDS 55

RESULT 12
US-08-511-485-6
Sequence 6, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-6

Query Match 98.0%; Score 301; DB 2; Length 604;
Best Local Similarity 98.2%; Pred. No. 6.4e-35;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVKCFCCGMLDNKRLGDS 55
DB 28 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVKCFCCGMLDNKRLGDS 82

RESULT 13
US-09-212-971-6
Sequence 6, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 604
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-6

Query Match 98.0%; Score 301; DB 3; Length 604;
Best Local Similarity 98.2%; Pred. No. 6.4e-35;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVKCFCCGMLDNKRLGDS 55
DB 28 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVKCFCCGMLDNKRLGDS 82

RESULT 14
US-08-800-929A-6
Sequence 6, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP

STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-6

Query Match 98.0%; Score 301; DB 4; Length 604;
Best Local Similarity 98.2%; Pred. No. 6.4e-35;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTFPAGVPYSESLARAGFYTGVDKVKCFCCGLMDNWKLGDSP 55
DB 28 CELYRMSTYSTFPAGVPYSESLARAGFYTGVDKVKCFCCGLMDNWKRGDSP 82

RESULT 15
US-08-569-749-4
Sequence 4, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-4

Query Match 98.0%; Score 301; DB 4; Length 604;
Best Local Similarity 98.2%; Pred. No. 6.4e-35;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTFPAGVPYSESLARAGFYTGVDKVKCFCCGLMDNWKLGDSP 55
DB 28 CELYRMSTYSTFPAGVPYSESLARAGFYTGVDKVKCFCCGLMDNWKRGDSP 82

Search completed: May 5, 2003, 16:09:09
Job time: 4.73848 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 3.12673 Seconds
(without alignments)
432.866 Million cell updates/sec

Title: US-08-569-749-7
Perfect score: 269
Sequence: 1 LARAGFYIIGPDRVACGACGKLSNWEPKDAMSEHRRHPNCPF 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269	100.0	46	US-08-569-749-7	Sequence 7, Appli
2	269	100.0	46	PCT-US96-12860-7	Sequence 7, Appli
3	269	100.0	67	US-08-511-485-23	Sequence 23, Appli
4	269	100.0	438	PCT-US95-05922A-2	Sequence 2, Appli
5	269	100.0	618	US-08-511-485-8	Sequence 8, Appli
6	269	100.0	618	US-08-212-971-8	Sequence 8, Appli
7	269	100.0	618	US-08-800-929A-8	Sequence 8, Appli
8	269	100.0	618	US-08-569-749-2	Sequence 2, Appli
9	269	100.0	618	US-08-617-053A-8	Sequence 8, Appli
10	269	100.0	618	US-09-069-023-29	Sequence 29, Appli
11	269	100.0	618	PCT-US96-12860-2	Sequence 2, Appli
12	269	100.0	612	US-09-212-971-14	Sequence 14, Appli
13	269	100.0	612	US-08-800-929A-14	Sequence 14, Appli
14	269	100.0	612	US-08-569-749-14	Sequence 14, Appli
15	269	100.0	612	US-08-617-053A-14	Sequence 14, Appli
16	269	100.0	612	PCT-US96-12860-14	Sequence 14, Appli
17	269	100.0	612	PCT-US96-12860-14	Sequence 14, Appli
18	269	100.0	612	US-08-511-485-22	Sequence 22, Appli
19	269	100.0	612	US-08-511-485-6	Sequence 6, Appli
20	269	100.0	612	US-09-212-971-6	Sequence 6, Appli
21	269	100.0	612	US-08-800-929A-6	Sequence 6, Appli
22	269	100.0	612	US-09-617-053A-6	Sequence 6, Appli
23	269	100.0	612	US-08-569-749-8	Sequence 8, Appli
24	269	100.0	612	US-08-569-749-8	Sequence 8, Appli
25	269	100.0	612	US-08-569-749-8	Sequence 8, Appli
26	269	100.0	612	US-08-569-749-8	Sequence 8, Appli
27	269	100.0	612	US-08-569-749-8	Sequence 8, Appli

28	241	89.6	600	4	US-09-617-053A-12	Sequence 12, Appli
29	192	71.4	68	2	US-08-511-485-21	Sequence 21, Appli
30	192	71.4	497	2	US-08-511-485-4	Sequence 4, Appli
31	192	71.4	497	3	US-09-212-971-4	Sequence 4, Appli
32	192	71.4	497	4	US-08-800-929A-4	Sequence 4, Appli
33	192	71.4	497	4	US-08-617-053A-4	Sequence 4, Appli
34	187	69.5	68	2	US-08-511-485-20	Sequence 20, Appli
35	187	69.5	496	2	US-08-511-485-10	Sequence 10, Appli
36	187	69.5	496	3	US-09-212-971-10	Sequence 10, Appli
37	187	69.5	496	4	US-08-800-929A-10	Sequence 10, Appli
38	187	69.5	496	4	US-09-617-053A-10	Sequence 10, Appli
39	187	69.5	236	4	US-09-121-979-4	Sequence 4, Appli
40	155	57.6	236	4	US-09-332-319-4	Sequence 4, Appli
41	155	57.6	236	4	US-09-239-867-2	Sequence 2, Appli
42	151	56.1	66	2	US-08-511-485-25	Sequence 25, Appli
43	151	56.1	236	4	US-09-239-867-4	Sequence 4, Appli
44	150	55.8	66	2	US-08-511-485-24	Sequence 24, Appli
45	149	55.4	1151	3	US-08-836-134-23	Sequence 23, Appli

ALIGNMENTS

RESULT 1
US-08-569-749-7
Sequence 7, Application US/08569749
Patent No: 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-7

Query Match 100.0%; Score 269; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.3e-28;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACGACGKLSNWEPKDAMSEHRRHPNCPF 46
DB 1 LARAGFYIIGPDRVACGACGKLSNWEPKDAMSEHRRHPNCPF 46

RESULT 2
PCT-US96-12860-7
Sequence 7, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-7

Query Match 100.0%; Score 269; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.3e-28;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46

RESULT 3
US-08-511-485-23
Sequence 23, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-23

Query Match 100.0%; Score 269; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 6.4e-28;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 21 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 66

RESULT 4
PCT-US95-05922A-2
Sequence 2, Application PC/TUS9505922A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922A
FILING DATE: 11 MAY 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-292
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-05922A-2

Query Match 100.0%; Score 269; DB 5; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.7e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 46
|||||
DB 24 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 69

RESULT 5
US-08-511-485-8
Sequence 8, Application US/08511485
Patent No. 5919912

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906

TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-8

Query Match 100.0%; Score 269; DB 2; Length 618;
Best Local Similarity 100.0%; Pred. No. 6.8e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 46
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DB 204 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 249

RESULT 6
US-09-212-971-8
Sequence 8, Application US/09212971B
Patent No. 6107041

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
EARLIER FILING DATE: 1998-12-16
CURRENT FILING DATE: 1998-04-26
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1997-02-13
EARLIER APPLICATION NUMBER: 08/800,929
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-8

Query Match 100.0%; Score 269; DB 3; Length 618,
Best Local Similarity 100.0%; Pred. No. 6.8e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 46
|||||
DB 204 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 249

RESULT 7
US-08-800-929A-8
Sequence 8, Application US/08800929A
Patent No. 6133437

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045

```

;
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-929A-8

Query Match          100.0%; Score 269; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 6.8e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 249

RESULT 8
US-08-569-749-2.
; Sequence 2, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Goeddel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,749
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-569-749-2

Query Match          100.0%; Score 269; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 6.8e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 249

RESULT 9
US-09-617-053A-8
; Sequence 8, Application US/09617053A
; Patent No. 6300492

;
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-617-053A-8

Query Match          100.0%; Score 269; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 6.8e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 249

RESULT 10
US-09-069-023-29
; Sequence 29, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-069-023-29

Query Match          100.0%; Score 269; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 6.8e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 249

RESULT 11
PCT-US96-12860-2
; Sequence 2, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
```

STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-2

Query Match 100.0%; Score 269; DB 5; Length 618;
Best Local Similarity 100.0%; Pred. No. 6.8e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 249

RESULT 12
US-09-212-971-14
Sequence 14, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE:
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 612
TYPE: PRT
ORGANISM: Mus musculus
US-09-212-971-14

Query Match 98.1%; Score 264; DB 3; Length 612;
Best Local Similarity 97.8%; Pred. No. 3e-26;

Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 46
DB 197 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 242

RESULT 13
US-08-800-929A-14
Sequence 14, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-14

Query Match 98.1%; Score 264; DB 4; Length 612;
Best Local Similarity 97.8%; Pred. No. 3e-26;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 46
DB 197 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 242

RESULT 14
US-08-569-749-14
Sequence 14, Application US/08569749
Patent No. 6187557

GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-14

Query Match 98.1%; Score 264; DB 4; Length 612;
Best Local Similarity 97.8%; Pred. No. 3e-26;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
|||||
DB 197 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 242

RESULT 15
US-09-617-053A-14
Sequence 14, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 612
TYPE: PRT
ORGANISM: Mus musculus
US-09-617-053A-14

Query Match 98.1%; Score 264; DB 4; Length 612;
Best Local Similarity 97.8%; Pred. No. 3e-26;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
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DB 197 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 242

Search completed: May 5, 2003, 16:09:10
Job time: 3.12673 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:50:57 ; Search time 9.06221 Seconds

(without alignments)
676.383 Million cell updates/sec

Title: US-08-569-749-7

Perfect score: 269
Sequence: 1 LARAGFYIGPGDRVACFAC.....WEPRKDAMSEHRRHFPNCPF 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	269	100.0	46	18	AAW13549	Human c-IAP1 repa
2	269	100.0	438	17	AAW04583	Human inhibitor of
3	269	100.0	618	18	AAW19746	Human inhibitor of
4	269	100.0	618	18	AAW19583	Human apoptosis in
5	269	100.0	618	18	AAW13545	Human c-IAP1. Hom
6	269	100.0	618	19	AAW69296	Human HIAP-2 prote
7	269	100.0	618	20	AAW33998	Human cellular inh
8	269	100.0	618	23	ABG65665	Human inhibitor of
9	264	98.1	612	18	AAW13555	Murine c-IAP. Mus
10	264	98.1	612	19	AAW69299	Murine HIAP-2 prot

11	257	95.5	306	22	AAU02925	Angiotensin conver
12	255	94.8	591	18	AAW19586	Mouse apoptosis in
13	255	94.8	591	23	ABG65668	Mouse inhibitor of
14	251	93.3	604	18	AAW19582	Human apoptosis in
15	251	93.3	604	19	AAW69295	Human HIAP-1 prote
16	251	93.3	604	23	ABG65664	Human inhibitor of
17	248	92.2	46	18	AAW13550	Human c-IAP2 repa
18	248	92.2	604	18	AAW19747	Human inhibitor of
19	248	92.2	604	18	AAW13546	Human c-IAP2. Hom
20	248	92.2	604	20	AAV52703	Human cellular inh
21	248	92.2	604	20	AAV33997	Human cellular inh
22	248	92.2	1140	23	AAU97837	Human cysteine pro
23	248	92.2	1141	22	AAW50694	Human API2-MIT chl
24	241	89.6	600	19	AAW69298	Murine HIAP-1 prot
25	241	89.6	602	18	AAW19585	Mouse apoptosis in
26	241	89.6	602	23	ABG65667	Mouse inhibitor of
27	192	71.4	497	18	AAW19581	Human apoptosis in
28	192	71.4	497	19	AAW69294	Human XIAP protein
29	192	71.4	497	21	AAV99985	Human X-linked inh
30	192	71.4	497	21	AAV59451	Human XIAP protein
31	192	71.4	497	23	ABG65663	Human inhibitor of
32	188	69.9	464	23	AAU75747	Human inhibitor of
33	187	69.5	496	18	AAW19745	Mouse apoptosis in
34	187	69.5	496	18	AAW19584	Mouse apoptosis in
35	187	69.5	496	19	AAW69297	Murine XIAP protei
36	187	69.5	496	23	ABG65666	Mouse inhibitor of
37	155	57.6	236	21	AAW81440	Human TIAP (an inh
38	155	57.6	236	22	AAE00365	Human IAP-like pro
39	155	57.6	236	22	AAE00366	Human IAP-like pro
40	155	57.6	236	23	AAU75066	Human testes spect
41	154	57.2	236	22	AAE00367	Gorilla IAP-like p
42	151	56.1	278	23	AAO20511	Protein of APP rel
43	149	55.4	1232	17	AAW8217	Neuronal apoptosis
44	149	55.4	1295	20	AAW14080	Conadotropic hormo
45	149	55.4	1295	20	AAW09540	Human apoptosis in

ALIGNMENTS

RESULT 1
AAW13549
ID AAW13549 standard; Protein; 46 AA.
XX
AC AAW13549;
XX
DT 22-JUL-1997 (first entry)
XX
DE Human c-IAP1 repeat 2.
XX
KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;
KW myocardial infarction; nephritis; HIV.
XX
OS Homo sapiens.
XX
PN W09706182-A1.
XX
PD 20-FEB-1997.
XX
PF 06-AUG-1996; 96WO-US12860.
XX
PR 08-DEC-1995; 95US-0569749.
PR 08-AUG-1995; 95US-0512946.
XX
PA (TULIA-) TULARIK INC.
XX
PI Goeddel DV, Rothe M;
XX
DR WPI; 1997-154209/14.
XX
PT Nucleic acids encoding cellular inhibitor of apoptosis proteins
PT useful for apoptosis regulation in cells to reduce or increase
PT apoptosis and for pharmacological screening

XX Claim 3; Page 24; 35pp; English.

The human cellular inhibitor of apoptosis proteins (c-IAP1/2 - AAT61590/T61591) comprise a series of defined structural domain repeats and/or a RING finger domain; in particular, at least two of a first domain repeat (AAW13547 or AAW13548), a second domain repeat (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552) and/or a RING finger domain (AAW13553 or AAW13554), or a consensus sequences derived from these human genes.

The nucleic acid is used for recombinant prodn. of human cellular inhibitor of apoptosis protein which modulates apoptosis regulation. The nucleic acids are useful in therapies where increased cell-specific apoptosis is desired, e.g. In restinosis, inflammatory disease states, myocardial infarction, glomerular nephritis, transplant rejection and infectious diseases, e.g. HIV. They can also be used in conditions requiring a reduction in apoptosis.

Sequence 46 AA:

Query Match 100.0%; Score 269; DB 18; Length 46;
Best Local Similarity 100.0%; Pred. No. 1e-26;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEPKDDAMSEHRRHPNCPF 46
|||||
DB 1 LARAGFYIIGPDRVACFACGKLSNWEPKDDAMSEHRRHPNCPF 46

RESULT 2
AAW04583
ID AAW04583 standard; Protein; 438 AA.
XX AAW04583;
AC
XX
DT 07-FEB-1997 (first entry)
XX
XX
DE Human inhibitor of apoptosis gene 1.
XX
KW Inhibitor of apoptosis 1; hIAP-1; degenerative disease;
KV rheumatoid arthritis; septic shock; antiviral; trauma; stroke;
KW cell death; oncogenesis; cancer; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN MO9635703-A1.
PD
XX 14-NOV-1996.
PF 11-MAY-1995; 95WO-US05922.
XX
PR 11-MAY-1995; 95WO-US05922.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PT He WM, Hudson PL, Rosen CA;
XX MPI; 1996-518608/51.
DR N-PSTB; AAT43709.
XX
PT Polynucleotide encoding human inhibitor of apoptosis gene 1 - useful
PT for treating degenerative diseases, as antiviral defence mechanism
XX and preventing cell death during trauma and strokes
XX
PS Claim 1; Page 40-41; 53pp; English.
XX
CC Human inhibitor of apoptosis 1 (hIAP-1) (AAW04583) is a protein
CC useful for treating degenerative diseases, rheumatoid arthritis,
CC septic shock, as an antiviral defence mechanism, and for
CC preventing cell death during strokes or trauma. Its amino acid
CC sequence was deduced from a cDNA clone (AAT43709) that can be obt.
CC from human Jurkat cell lines or human osteoclastoma stromal cell

```
CC      lines. Recombinant hIAP-1 can be produced in prokaryotic or
CC      eukaryotic host cells, or expressed in vivo. It can also be used
CC      to screen for modulators of hIAP-1 activity.
XX      SQ      Sequence      438 AA;
QY      1 LARAGFYITIGPDRVACFACGCKLSNNEPKDDAMSEHRRHFPCPF 46
DB      24 LARAGFYITIGPDRVACFACGCKLSNNEPKDDAMSEHRRHFPCPF 69

RESULT 3
AAW19746
AAW19746 standard; Protein; 618 AA.
AAW19746;
16-SEP-1997 (first entry)
Human inhibitor of apoptosis protein homologue MIHB.
Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHB;
degenerative-disease; infectious disease; autoimmune disease;
cancer; therapy; diagnosis.
Homo sapiens.
OS
XX
XX
FH      Key      Location/Qualifiers
FT      Region      46..113
FT      /label= BIR
FT      Region      184..250
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FT      Region      269..337
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FT      Region      569..606
FT      /label= RING_finger
XX
XX
PN      W09723501-A1.
PD      03-JUL-1997.
XX
XX      20-DEC-1996; 96WO-AU00827.
PE
PR      22-DEC-1995; 95AU-0007275.
XX
PA      (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI      Vaux DL;
XX
XX      WPI; 1997-350966/32.
DR      N-PSDB; AAT72711.
XX
PT      Isolated protein homologues of viral inhibitors of apoptosis - used
PT      to modulate apoptosis for treatment of degenerative, infectious or
PT      autoimmune diseases and cancer
XX
PS      Claim 8; Page 51-54; 136pp; English.
XX
XX      Mammalian IAP homologue B (MIHB) (AAW19746) is a human homologue of
CC      baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
CC      sequence was deduced from a cDNA clone (see also AAT72711) isolated
CC      from a human foetal liver cDNA library using primers based on
CC      human EST sequences that resembled the BIR repeats of Oryza
CC      pseudosugura polyhedrosis virus IAP. IAP homologues (see also
CC      AAW19745 and AAW19747-52) and their derivatives and chemical analogues
CC      can be used in methods for modulating apoptosis in animal cells,
CC      specifically for treatment, by inhibition, of degenerative and
CC      infectious disease or, by promotion, of cancer and autoimmune
CC      disease.
```

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XX      SQ      Sequence      618 AA;
XX      Query Match      100.0%; Score 269; DB 18; Length 618;
XX      Best Local Similarity 100.0%; Pred. No. 1.6e-25;
XX      Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 LARAGFYIIGPDGVACFACGKLSNWEPKDAMSEHRRHPNCPF 46
      |||
      204 LARAGFYIIGPDGVACFACGKLSNWEPKDAMSEHRRHPNCPF 249

RESULT 4
AAW19583
ID      AAW19583 standard; Protein; 618 AA.
XX
AC      AAW19583;
XX
DT      02-SEP-1997 (first entry)
XX
DE      Human apoptosis inhibitor HIAP-2.
XX
KW      Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration;
KW      myelodysplastic syndrome; ischemia; myocardial infarction; stroke;
KW      reperfusion injury; toxin-induced liver disease; gene therapy;
KW      diagnosis.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FH      Domain      46..113
FH      FT      /label= BIR-1
FH      FT      184..250
FH      FT      /label= BIR-2
FH      FT      269..336
FH      FT      /label= BIR-3
FH      FT      560..605
FH      FT      /label= Ring_zinc_finger
XX
PN      WO9706255-A2.
XX
PD      20-FEB-1997.
XX
PF      05-AUG-1996; 96WO-IB01022.
XX
PR      22-DEC-1995; 95US-0576956.
PR      04-AUG-1995; 95US-0511485.
XX
PA      (UYOT-) UNIV OTTAWA.
XX
PI      Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX
XX      WPI: 1997-154262/14.
XX      N-PSDB; AAT70838.
XX
PT      Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT      to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT      of susceptibility to apoptotic disease
XX
PS      Claim 27; Page 75-77; 219pp; English.
XX
XX      Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
XX      M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
XX      are inhibitors of apoptosis (IAP) and which are characterised by
XX      the presence of a ring zinc finger domain (see also AAW19587) and at
XX      least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
XX      The HIAP amino acid sequences were deduced from cDNA clones (AAT70837
XX      and AAT70838) from a human liver library. IAP polypeptides can be
XX      expressed in host cells (in vitro or in vivo) and used in methods
XX      for treating diseases and disorders involving apoptosis, esp. in a
XX      human diagnosed as HIV-positive or as having AIDS, a
XX      neurodegenerative disease, a myelodysplastic syndrome or an
XX      ischaemic injury, selected from myocardial infarction, stroke,

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CC      reperfusion injury, or a toxin-induced liver disease.
XX
XX      SQ      Sequence      618 AA;
XX      Query Match      100.0%; Score 269; DB 18; Length 618;
XX      Best Local Similarity 100.0%; Pred. No. 1.6e-25;
XX      Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 LARAGFYIIGPDGVACFACGKLSNWEPKDAMSEHRRHPNCPF 46
      |||
      204 LARAGFYIIGPDGVACFACGKLSNWEPKDAMSEHRRHPNCPF 249

RESULT 5
AAW13545
ID      AAW13545 standard; Protein; 618 AA.
XX
AC      AAW13545;
XX
DT      22-JUL-1997 (first entry)
XX
DE      Human c-IAP1.
XX
KW      IAP; inhibitor; apoptosis; RING finger domain; restinosis;
KW      myocardial infarction; nephritis; HIV.
XX
OS      Homo sapiens.
XX
PN      WO9706182-A1.
XX
PD      20-FEB-1997.
XX
PF      06-AUG-1996; 96WO-US12860.
XX
PR      08-DEC-1995; 95US-0569749.
PR      08-AUG-1995; 95US-0512946.
XX
PA      (TULA-) TULARIK INC.
XX
PI      Goeddel DV, Rothe M;
XX
XX      WPI: 1997-154209/14.
XX      N-PSDB; AAT61590.
XX
PT      Nucleic acids encoding cellular inhibitor of apoptosis proteins -
PT      useful for apoptosis regulation in cells to reduce or increase
PT      apoptosis and for pharmacological screening
XX
PS      Disclosure; Page 18-20; 35pp; English.
XX
XX      The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
XX      AAT61590/T61591) comprise a series of defined structural domain
XX      repeats and/or a RING finger domain; in particular, at least two of
XX      a first domain repeat (AAW13547 or AAW13548), a second domain repeat
XX      (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
XX      and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
XX      sequence derived from these human genes.
XX      The nucleic acid is used for recombinant prodn. of human cellular
XX      inhibitor of apoptosis protein which modulates apoptosis
XX      regulation. The nucleic acids are useful in therapies where
XX      increased cell-specific apoptosis is desired, e.g. in restinosis,
XX      inflammatory disease states, myocardial infarction, glomerular
XX      nephritis, transplant rejection and infectious diseases, e.g. HIV.
XX      They can also be used in conditions requiring a reduction in
XX      apoptosis.
XX
XX      SQ      Sequence      618 AA;
XX
XX      Query Match      100.0%; Score 269; DB 18; Length 618;
XX      Best Local Similarity 100.0%; Pred. No. 1.6e-25;
XX      Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 LARAGFYIIGPDGVACFACGKLSNWEPKDAMSEHRRHPNCPF 46

```

Db 204 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 249

RESULT 6
AAW69296 standard; Protein; 618 AA.

AC AAW69296;

DT 13-NOV-1998 (first entry)

DE Human HIAP-2 protein.

KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein.

OS Homo sapiens.

PN W09835693-A2.

PD 20-AUG-1998.

PF 13-FEB-1998; 98WO-IB00781.

PR 13-FEB-1997; 97US-0800929.

PA (UYOT-) UNIV OTTAWA.

PI Baird S, Korneluk R, Liston P, Mackenzie AI, Pratt C;
PI Tsang B;

DR WPI; 1998-467164/40.

DR N-PSDB; AAV55040.

PT Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations

PS Disclosure; Fig 3; 147pp; English.

CC This sequence is the human HIAP-2 protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.

SQ Sequence 618 AA;

Query Match 100.0%; Score 269; DB 19; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
Db 204 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 249

RESULT 7
AAV33998 standard; Protein; 618 AA.
ID AAV33998
XX

AC AAV33998;

DT 26-NOV-1999 (first entry)

DE Human cellular inhibitor of apoptosis-1 sequence.

KW Cellular inhibitor of Apoptosis-1; antisense; diagnostic; therapeutic;
KW c-IAP-1; prophylaxis; infection; inflammation; tumor formation.

OS Homo sapiens.

PN US958772-A.

PD 28-SEP-1999.

PF 03-DEC-1998; 98US-0205204.

PR 03-DEC-1998; 98US-0205204.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowsett LM, Ackermann EJ;

DR WPI; 1999-561047/47.

DR N-PSDB; AA222143.

PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-1
PT useful for e.g. diagnostics, therapeutics, and as research reagents -
PT Example 13; Columns 41-46; 32pp; English.

CC The invention provides antisense compounds of 8-30 nucleotides that
CC inhibit the expression of human cellular inhibitor of Apoptosis-1
CC (c-IAP-1). The antisense compounds may be used for diagnostics,
CC therapeutics (for modulating the expression of c-IAP-1), prophylaxis
CC (e.g. to prevent or delay infection, inflammation, or tumor formation),
CC as research reagents (e.g. to distinguish between members of a biological
CC pathway) and in kits. The present sequence represents the human cellular
CC inhibitor of apoptosis-1.

SQ Sequence 618 AA;

Query Match 100.0%; Score 269; DB 20; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
Db 204 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 249

RESULT 8

ABG65665 standard; Protein; 618 AA.

AC ABG65665;

DT 26-AUG-2002 (first entry)

DE Human inhibitor of apoptosis, HIAP2.

KW Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.

OS Homo sapiens.

PN W0200226968-A2.

PD 04-APR-2002.

XX 27-SEP-2001; 2001WO-CA01379.
XX
XX 28-SEP-2000; 2000US-0672717.
XX
XX (UYOT-) UNIV OTTAWA.
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX WPI: 2002-479562/51.
XX N-PSDB; ABR33871.
XX
XX Novel antisense inhibitor of apoptosis nucleic acid useful for
XX enhancing apoptosis in a cell, for treating cancer and other
XX proliferative diseases
XX
XX Disclosure; Fig 3; 135pp; English.
XX
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
XX nucleic acid (I) that inhibits IAP biological activity, regardless of
XX length of the antisense nucleic acid, the IAP proteins may be mouse
XX or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
XX composition comprising a mammalian IAP antisense molecule and a method of
XX enhancing apoptosis in a cell, comprising administering a negative
XX regulator of the IAP anti-apoptotic pathway to the cell. The IAP
XX antisense inhibitor is useful for enhancing apoptosis in a cell in a
XX mammal diagnosed with a proliferative disease. The method is useful for
XX treating a patient diagnosed with a proliferative disease like cancer.
XX The IAP antisense molecule is useful to treat, ameliorate, improve,
XX sustain or prevent proliferative diseases (e.g. ovarian cancer,
XX adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
XX conditions where apoptosis is involved or implicated (e.g. embryonic
XX development, viral pathogenesis, autoimmune disorders, neurodegenerative
XX diseases, multiple sclerosis, lupus erythematosus and infection by herpes
XX virus, pox virus and adenovirus). The present sequence is a human IAP
XX protein sequence.
XX
SQ Sequence 618 AA;

Query Match 100.0%; Score 269; DB 23; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 249

RESULT 9
AAW13555
ID AAW13555 standard; Protein: 612 AA.
XX
XX AAW13555;
XX
XX 22-JUL-1997 (first entry)
XX
XX Murine c-IAP.
XX
XX IAP; inhibitor; apoptosis; RING finger domain; restinosis;
XX myocardial infarction; nephritis; HIV.
XX
XX Mus musculus.
XX
XX W09706182-A1.
XX
XX 20-FEB-1997.
XX
XX 06-AUG-1996; 96WO-US12860.
XX
XX 08-DEC-1995; 95US-0569749.
XX
XX 08-AUG-1995; 95US-0512946.
XX

PA (TULA-) TULARIK INC.
XX
XX Goeddel DV, Rothe M;
XX
XX WPI: 1997-154209/14.
XX N-PSDB; AAT61592.
XX
XX
XX Nucleic acids encoding cellular inhibitor of apoptosis proteins
XX useful for apoptosis regulation in cells to reduce or increase
XX apoptosis and for pharmacological screening
XX
XX Disclosure; Page 28-29; 35pp; English.
XX
XX
XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
XX AAT61590/T61591) comprise a series of defined structural domain
XX repeats and/or a RING finger domain; in particular, at least two of
XX a first domain repeat (AAW13547 or AAW13548), a second domain repeat
XX (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
XX and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
XX sequences derived from these human genes.
XX The nucleic acid is used for recombinant prodn. of human cellular
XX inhibitor of apoptosis protein which modulates apoptosis
XX regulation. The nucleic acids are useful in therapies where
XX increased cell-specific apoptosis is desired, e.g. in restinosis,
XX inflammatory disease states, myocardial infarction, glomerular
XX nephritis, transplant rejection and infectious diseases, e.g. HIV.
XX They can also be used in conditions requiring a reduction in
XX apoptosis.
XX
SQ Sequence 612 AA;

Query Match 98.1%; Score 264; DB 18; Length 612;
Best Local Similarity 97.8%; Pred. No. 6.6e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 197 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 242

RESULT 10
AAW69299
ID AAW69299 standard; Protein: 612 AA.
XX
XX AAW69299;
XX
XX 13-NOV-1998 (first entry)
XX
XX Murine HIAP-2 protein.
XX
XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
XX proliferative disease; IAP; therapy; cancer; mouse; HIAP-2 protein.
XX
XX Mus sp.
XX
XX W09835693-A2.
XX
XX 20-AUG-1998.
XX
XX 13-FEB-1998; 98WO-IB00781.
XX
XX 13-FEB-1997; 97US-0800929.
XX
XX (UYOT-) UNIV OTTAWA.
XX
XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
XX Tsang B;
XX
XX WPI: 1998-467164/40.
XX N-PSDB; AAV55043.
XX
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
XX of IAP or NAIP polypeptide - also methods for prognosis based on
XX

PT Presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations
XX
XX
XX Disclosure: Fig 6; 147pp; English.
XX
CC This sequence is the murine HIAP-2 protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.
XX
SQ Sequence 612 AA;
Query Match 98.1%; Score 264; DB 19; Length 612;
Best Local Similarity 97.8%; Pred. No. 6.6e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 LARAGFYIIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
Db 197 LARAGFYIIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCPF 242
RESULT 11
AAU02925
ID AAU02925 standard; Protein; 306 AA.
XX
XX AAU02925;
XX
XX 12-SEP-2001 (first entry)
XX
XX Angiotensin converting enzyme (ACEV) splice variant protein #25.
DE
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonarctoidic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.
XX
XX Homo sapiens.
XX
XX WO200136632-A2.
XX
XX 25-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-IL00766.
XX
XX 17-NOV-1999; 99IL-0132978.
XX
XX 10-DEC-1999; 99IL-0133455.
XX
XX (COMP-) COMPUGEN LTD.
XX
XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX
XX MPI: 2001-336004/35.
XX
XX N-PSDB; AAS06025.
XX
XX Novel alternative splicing variants e.g. variant of angiotensin
XX converting enzyme (ACEV), useful in identifying candidate compounds
XX

PT capable of binding to the variant and to detect anti-variant antibodies
PT
XX
XX Claim 4; Fig 25; 519pp; English.
XX
XX
CC The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, nonarctoidic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis.
XX
SQ Sequence 306 AA;
Query Match 95.5%; Score 257; DB 22; Length 306;
Best Local Similarity 95.7%; Pred. No. 2.4e-24;
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 LARAGFYIIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
Db 204 LARAGFYIIGPDRAVACFACGKLSNWEKDDAMSEHRRHFPNCPF 249
RESULT 12
AAW19586
ID AAW19586 standard; Protein; 591 AA.
XX
XX AAW19586;
XX
XX 02-SEP-1997 (first entry)
XX
XX Mouse apoptosis inhibitor M-HIAP-2.
DE
XX Apoptosis inhibitor; M-HIAP-2; HIV; AIDS; neurodegeneration;
KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
KW diagnosis.
XX
XX Mus sp.
XX
XX
XX key Location/Qualifiers
FH Domain 25..92
FT /label= BIR-1
FT Domain 156..222
FT /label= BIR-2
FT Domain 241..308
FT /label= BIR-3
FT Domain 541..578
FT /label= Ring_zinc_finger
XX
XX WO9706255-A2.
XX
XX 20-FEB-1997.
XX
XX 05-AUG-1996; 96WO-IB01022.
XX
XX 22-DEC-1995; 95US-0576956.
XX
XX 04-AUG-1995; 95US-0511485.
XX
XX (UYOT-) UNIV OTTAWA.
XX
XX Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX

DR WPI, 1997-154262/14.
DR N-PSDB; AAT70841.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT of susceptibility to apoptotic disease
XX
PS Claim 30; Page 100-102; 219pp; English.
XX
CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterised by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The M-HIAP amino acid sequences were deduced from isolated m-hiap
CC cDNA clones (AAT70840-41). IAP polypeptides can be expressed in host
CC cells (in vitro or in vivo) and used in methods for treating
CC diseases and disorders involving apoptosis, esp. in a human
CC diagnosed as HIV-positive or as having AIDS, a neurodegenerative
CC disease, a myelodysplastic syndrome or an ischaemic injury, selected
CC from myocardial infarction, stroke, reperfusion injury, or a toxin-
CC induced liver disease.
XX
SQ Sequence 591 AA;
Query Match 94.8%; Score 255; DB 18; Length 591;
Best Local Similarity 95.7%; Pred. No. 8.7e-24;
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 46
DB 176 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 221
|||||
RESULT 13
ABG65668
ID ABG65668 standard; Protein; 591 AA.
XX
AC ABG65668;
XX
DT 26-AUG-2002 (first entry)
XX
DE Mouse inhibitor of apoptosis, HIAP2.
XX
KW Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cyrostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX
OS Mus sp.
XX
PN WO200226968-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-CA01379.
XX
PR 28-SEP-2000; 2000US-0672717.
XX
PA (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX
DR WPI, 2002-479562/51.
DR N-PSDB; ABK93874.
XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for
PT enhancing apoptosis in a cell, for treating cancer and other
PT proliferative diseases
XX

PS Disclosure; Fig 6; 135pp; English.
XX
CC The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
CC protein sequence.
XX
SQ Sequence 591 AA;
Query Match 94.8%; Score 255; DB 23; Length 591;
Best Local Similarity 95.7%; Pred. No. 8.7e-24;
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 46
DB 176 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHPNCPF 221
|||||
RESULT 14
AAW19582
ID AAW19582 standard; Protein; 604 AA.
XX
AC AAW19582;
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor HIAP-1.
XX
KW Apoptosis inhibitor; HIAP-1; HIV; AIDS; neurodegeneration;
KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
KW diagnosis.
XX
OS Homo sapiens.
XX
FH Key
FH Domain
FT 29..96 Location/Qualifiers
FT /label= BIR-1
FT 169..235
FT /label= BIR-2
FT 255..322
FT /label= BIR-3
FT 546..591
FT /label= Ring_zinc_finger
XX
PN WO9706255-A2.
XX
PD 20-FEB-1997.
XX
PF 05-AUG-1996; 96WO-IB01022.
XX
PR 22-DEC-1995; 95US-0576956.
PR 04-AUG-1995; 95US-0511485.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX
DR WPI, 1997-154262/14.

DR N-PSDB; AAT70837.
XX
XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT of susceptibility to apoptotic disease
XX
XX Claim 27; Page 72-74; 219pp; English.
XX
XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterised by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The IAP amino acid sequences were deduced from cDNA clones (AAT70837
CC and AAT70838) from a human liver library. IAP polypeptides can be
CC expressed in host cells (in vitro or in vivo) and used in methods
CC for treating diseases and disorders involving apoptosis, esp. in a
CC human diagnosed as HIV-positive or as having AIDS, a
CC neurodegenerative disease, a myelodysplastic syndrome or an
CC ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease.
XX
SQ Sequence 604 AA;

Query Match 93.3%; Score 251; DB 18; Length 604;
Best Local Similarity 93.5%; Pred. No. 2.9e-23;
Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGDRVACFACGKLSNWEPKDAMSEHRRHFPNCPF 46
DB 189 LARAGFYIIGPGDRVACFACGKLSNWEPKDAMSEHRRHFPNCPF 234
|||||

RESULT 15
AAW69295
ID AAW69295 standard; Protein; 604 AA.
XX
AC AAW69295;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human HIAP-1 protein.
XX
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
XX proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein.
OS Homo sapiens.
XX
PN WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB00781.
XX
PR 13-FEB-1997; 97US-0800929.
XX
XX (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
PI Tsang B;
XX
DR WPI; 1998-467164/40.
DR N-PSDB; AAV55039.
XX
XX
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations
XX
XX
PS Disclosure; Fig 2; 147pp; English.
XX
CC This sequence is the human HIAP-1 protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.

CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.
XX
SQ Sequence 604 AA;

Query Match 93.3%; Score 251; DB 19; Length 604;
Best Local Similarity 93.5%; Pred. No. 2.9e-23;
Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGDRVACFACGKLSNWEPKDAMSEHRRHFPNCPF 46
DB 189 LARAGFYIIGPGDRVACFACGKLSNWEPKDAMSEHRRHFPNCPF 234
|||||

Search completed: May 5, 2003, 16:02:00
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:07 ; Search time 5.67051 Seconds
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Title: US-08-569-749-7
Perfect score: 269
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NIM_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	269	100.0	67	9	US-09-201-936-23
2	269	100.0	438	1	US-08-464-588-2
3	269	100.0	618	9	US-09-201-936-8
4	269	100.0	618	10	US-09-974-592-8
5	264	98.1	612	10	US-09-974-592-14
6	257	95.5	306	10	US-09-778-927A-62
7	255	94.8	591	9	US-09-201-936-42
8	251	93.3	67	9	US-09-201-936-22
9	251	93.3	604	9	US-09-201-936-6
10	251	93.3	604	10	US-09-974-592-6
11	241	89.6	600	10	US-09-974-592-12
12	241	89.6	602	9	US-09-201-936-40
13	192	71.4	68	9	US-09-201-936-21
14	192	71.4	110	9	US-09-965-967-21
15	192	71.4	497	9	US-09-201-936-4
16	192	71.4	497	10	US-09-974-592-4
17	187	69.5	68	9	US-09-201-936-20
18	187	69.5	496	9	US-09-201-936-10
19	187	69.5	496	10	US-09-974-592-10

20	151	56.1	66	9	US-09-201-936-25	Sequence 25, Appl
21	151	56.1	107	9	US-09-965-967-20	Sequence 20, Appl
22	151	56.1	278	9	US-09-964-899-39	Sequence 39, Appl
23	150	55.8	66	9	US-09-201-936-24	Sequence 24, Appl
24	149	55.4	1403	8	US-08-913-322-22	Sequence 22, Appl
25	149	55.4	1403	8	US-08-913-322-24	Sequence 24, Appl
26	140	52.0	67	9	US-09-201-936-15	Sequence 15, Appl
27	140	52.0	498	9	US-09-201-936-13	Sequence 13, Appl
28	139	51.7	68	9	US-09-201-936-19	Sequence 19, Appl
29	138	51.3	68	9	US-09-201-936-18	Sequence 18, Appl
30	138	51.3	68	9	US-09-201-936-27	Sequence 27, Appl
31	135	50.2	68	9	US-09-201-936-16	Sequence 16, Appl
32	132	49.1	68	9	US-09-201-936-26	Sequence 26, Appl
33	132	49.1	68	9	US-09-201-936-28	Sequence 28, Appl
34	132	49.1	68	9	US-10-041-859-18	Sequence 18, Appl
35	132	49.1	172	9	US-10-041-859-8	Sequence 8, Appl
36	132	49.1	172	9	US-10-041-859-12	Sequence 12, Appl
37	132	49.1	346	9	US-10-041-859-2	Sequence 2, Appl
38	131	48.7	68	9	US-09-201-936-17	Sequence 17, Appl
39	131	48.7	110	9	US-09-965-967-22	Sequence 22, Appl
40	129	48.0	67	9	US-09-201-936-11	Sequence 11, Appl
41	129	48.0	68	9	US-10-041-859-19	Sequence 19, Appl
42	129	48.0	109	9	US-09-965-967-30	Sequence 30, Appl
43	129	48.0	172	9	US-10-041-859-13	Sequence 13, Appl
44	128	47.6	109	9	US-09-965-967-19	Sequence 19, Appl
45	126	46.8	172	9	US-10-041-859-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-201-936-23
; Sequence 23, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluz, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.10
; SEQ ID NO 23
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-23

Query Match 100.0%; Score 269; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 4.7e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
|||||
Db 21 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 66

RESULT 2
US-08-464-588-2
; Sequence 2, Application US/08464588

```
Publication No. US20030073159A1
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,588
FILING DATE: June 5, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922
FILING DATE: 11 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-387
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-464-588-2

Query Match          100.0%; Score 269; DB 1; Length 438;
Best Local Similarity 100.0%; Pred. No. 3,5e-26;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 24 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 69

RESULT 3
US-09-201-936-8
Sequence 8, Application US/09201936
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
EARLIER FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
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SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-8

Query Match          100.0%; Score 269; DB 9; Length 618;
Best Local Similarity 100.0%; Pred. No. 5.1e-26;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 249

RESULT 4
US-09-974-592-8
Sequence 8, Application US/09974592
Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-974-592-8

Query Match          100.0%; Score 269; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 5.1e-26;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 249

RESULT 5
US-09-974-592-14
Sequence 14, Application US/09974592
Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
```

PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 612
TYPE: PRT
ORGANISM: Mus musculus
US-09-974-592-14

Query Match 98.1%; Score 264; DB 10; Length 612;
Best Local Similarity 97.8%; Pred. No. 2.2e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEPKDDAMSEHRRHFPNCPF 46
Db 197 LARAGFYIIGPDRVACFACGKLSNWEPKDDAMSEHRRHFPNCPF 242

RESULT 6
US-09-778-927A-62

Sequence 62, Application US/09778927A
Patent No. US20020068342A1

GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Ramt et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: IL134453
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
LENGTH: 306
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(306)
OTHER INFORMATION: xaa - any amino acid, unknown, or other
US-09-778-927A-62

Query Match 95.5%; Score 257; DB 10; Length 306;
Best Local Similarity 95.7%; Pred. No. 7.9e-25;
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEPKDDAMSEHRRHFPNCPF 46
Db 204 LARAGFYIIGPDRVACFACGKLSNWEPKDDAMSEHRRHFPNCPF 249

RESULT 7
US-09-201-936-42

Sequence 42, Application US/09201936
Publication No. US20020187946A1

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05

EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42
LENGTH: 591
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-936-42

Query Match 94.8%; Score 255; DB 9; Length 591;
Best Local Similarity 95.7%; Pred. No. 2.9e-24;
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEPKDDAMSEHRRHFPNCPF 46
Db 176 LARAGFYIIGPDRVACFACGKLSNWEPKDDAMSEHRRHFPNCPF 221

RESULT 8
US-09-201-936-22

Sequence 22, Application US/09201936
Publication No. US20020187946A1

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-22

Query Match 93.3%; Score 251; DB 9; Length 67;
Best Local Similarity 93.5%; Pred. No. 8.9e-25;
Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFACGKLSNWEPKDDAMSEHRRHFPNCPF 46
Db 21 LARAGFYIIGPDRVACFACGKLSNWEPKDDAMSEHRRHFPNCPF 66

RESULT 9
US-09-201-936-6

Sequence 6, Application US/09201936
Publication No. US20020187946A1

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936

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; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-201-936-6
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Query Match          93.3%; Score 251; DB 3; Length 604;
Best Local Similarity 93.5%; Pred. No. 9.5e-24;
Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 LARAGFYIIGPGDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
|||||
DB 189 LARAGFYIIGPGDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 234
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RESULT 10
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-974-592-6
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Query Match          93.3%; Score 251; DB 10; Length 604;
Best Local Similarity 93.5%; Pred. No. 9.5e-24;
Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 LARAGFYIIGPGDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
|||||
DB 189 LARAGFYIIGPGDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 234
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RESULT 11
; Sequence 12, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
```

```
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-974-592-12
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Query Match          89.6%; Score 241; DB 10; Length 600;
Best Local Similarity 89.1%; Pred. No. 1.7e-22;
Matches 41; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 1 LARAGFYIIGPGDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
|||||
DB 187 LARAGFYIIGPGDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 232
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RESULT 12
; Sequence 40, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-201-936-40
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```
Query Match          89.6%; Score 241; DB 9; Length 602;
Best Local Similarity 89.1%; Pred. No. 1.8e-22;
Matches 41; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 1 LARAGFYIIGPGDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 46
|||||
DB 189 LARAGFYIIGPGDRVACFACGKLSNWEPRKDDAMSEHRRHFPNCPF 234
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RESULT 13
; Sequence 21, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
```

```

1  APPLICANT: Kornejuk, Robert G.
2  APPLICANT: Mackenzie, Alexander E.
3  APPLICANT: Baird, Stephen
4  APPLICANT: Liston, Peter
5  TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
6  TITLE OF INVENTION: PROBES, AND DETECTION METHODS
7  FILE REFERENCE: 07891/003003
8  CURRENT APPLICATION NUMBER: US/09/201,936
9  CURRENT FILING DATE: 1998-12-01
10 EARLIER APPLICATION NUMBER: 09/011,356
11 EARLIER FILING DATE: 1998-02-04
12 EARLIER APPLICATION NUMBER: PCT/IB96/01022
13 EARLIER FILING DATE: 1996-08-05
14 EARLIER APPLICATION NUMBER: 08/576,956
15 EARLIER FILING DATE: 1995-12-22
16 EARLIER APPLICATION NUMBER: 08/511,485
17 EARLIER FILING DATE: 1995-08-04
18 NUMBER OF SEQ ID NOS: 45
19 SOFTWARE: FastSeq for Windows Version 3.0
20 SEQ ID NO 21
21 LENGTH: 68
22 TYPE: PRT
23 ORGANISM: Homo sapiens
24 US-09-201-936-21

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Query Match	71.4%;	Score 192;	DB 9;	length 68;
Best Local Similarity	73.9%;	Prod. No. 7e-17;		
Matches	34;	Conservative	1;	Mismatches 11; Indels 0; Gaps 0;

QY	1	LARAGFYITGPD	RVACFACGCGKLS	NNEPKDDAMSE	HRHFFNCP	46
DB	22	LASAGLYTGTGID	VOVCFCCGGCKL	NNPKDDAMSE	HRHFFNCP	67

```

RESULT 14
US-09-965-967-21
: Sequence 21, Application US/09965967
: Patent No. US20020177557A1
: GENERAL INFORMATION:
: APPLICANT: Shi, Yigong
: TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
: FILE REFERENCE: PU-0031 (01-1739-1)
: CURRENT APPLICATION NUMBER: US/09/965,967
: CURRENT FILING DATE: 2001-09-28
: PRIOR APPLICATION NUMBER: 60/236,574
: PRIOR FILING DATE: 2000-09-29
: PRIOR APPLICATION NUMBER: 60/256,830
: PRIOR FILING DATE: 2000-12-20
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 21
:
: LENGTH: 110
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
US-09-965-967-21

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Query Match	71.48;	Score 192;	DB 9;	length 110;
Best Local Similarity	73.9%;	Pred. No.	4.5e-17;	
Matches	34;	Conservative	1;	Mismatches 11; Indels 0; Gaps 0;
Oy	1	IARAGFYIGPGRVACFACGCKLSNMEPKDDAMSEHRRHFPCPF	46	
Db	36	LASAGLYTTGIDGVOCFCGGCKLKNMEPCDRAWSEHRRHFPCPF	81	

RESULT 15
US-09-201-936-4
Sequence 4, Application US/09201936
Publication No. US2002018796A1
GENERAL INFORMATION:
APPLICANT: Korneljuk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen

```

APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBER, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/1996/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-4

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[illegible]

Search completed: May 5, 2003, 16:11:05
Job time : 5.67051 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:58:42 ; Search time 5.03456 Seconds
(without alignments)
878.365 Million cell updates/sec

Title: US-08-569-749-7
Perfect score: 269
Sequence: 1 LARAGFYIIGPDRVACFAC.....WLPKDDAMSEHRHFPNCPF 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269	100.0	618	2 S68450	apoptosis inhibitor
2	256	95.2	358	2 JC5964	apoptosis inhibitor
3	251	93.3	604	2 S68449	apoptosis inhibitor
4	192	71.4	497	2 S69544	apoptosis inhibitor
5	149	55.4	1232	2 A55478	neuronal apoptosis
6	140	52.0	496	2 S68452	apoptosis inhibitor
7	140	52.0	497	2 S69545	apoptosis inhibitor
8	138	51.3	1447	2 T42628	neuronal apoptosis
9	133.5	49.6	4845	2 T31067	BIR repeat contain
10	132	49.1	268	2 T10304	inhibitor of apopt
11	132	49.1	268	2 A53989	apoptosis-inhibiti
12	127	47.2	298	2 JC7568	kidney inhibitor o
13	124	46.1	275	2 A45679	inhibitor-of-apopt
14	117	43.5	208	2 T03183	probable apoptosis
15	111	41.3	150	2 T78409	ORF MSV248 probabl
16	107	39.8	155	2 T30489	apoptosis inhibito
17	104	38.7	997	2 T43523	cut11 protein - fl
18	98	36.4	292	2 T41772	IAP1 orf27 - Bomby
19	96	35.7	286	2 D36828	orf13 protein - Au
20	93	34.6	275	2 T10310	apoptosis-inhibiti
21	80	29.7	249	2 H72858	apoptosis inhibito
22	80	29.7	249	2 T37471	IAP2 orf11 - Bomby
23	72	26.8	155	2 T37471	apoptosis inhibito
24	66.5	24.7	329	2 T28403	ORF MSV242 probabl
25	63.5	23.6	278	1 S25690	hup1 protein - Rho
26	63	23.4	234	2 T30427	probable apoptosis
27	63	23.4	308	2 T37474	apoptosis inhibito
28	58.5	21.7	284	1 A41382	UTP-glucose-1-phos
29	57	21.2	122	2 S09314	phospholipase A2 (

30	57	21.2	138	2 F48188	phospholipase A2 (
31	56.5	21.0	181	2 E36794	hypothetical prote
32	56	20.8	2111	2 T15390	hypothetical prote
33	55.5	20.6	340	2 AD0701	tetrahionate redu
34	55	20.4	357	2 T50696	DNA primase small
35	55	20.4	409	2 S72438	phosphatidylserine
36	55	20.4	838	2 A48440	ring-infected eryt
37	54.5	20.3	424	2 E30857	hypothetical prote
38	54.5	20.3	424	2 T10400	alkaline exonuclea
39	54.5	20.3	517	1 D37831	phenol 2-monooxyge
40	54	20.1	355	2 C64549	conserved hypothet
41	54	20.1	355	2 G71958	hypothetical prote
42	54	20.1	954	2 S57108	hypothetical prote
43	54	20.1	1004	2 JH0470	Na+/K+-exchanging
44	53.5	19.9	297	2 T39905	protein transport
45	53.5	19.9	525	1 S39834	myb-related protei

ALIGNMENTS

RESULT 1
S68450
apoptosis inhibitor hlap-2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68450
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAI1 and a related family of
A:Reference number: A58182; MID:96149249; PMID:8552191
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <LIS>
A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:567-611/Domain: RING finger homology <RNG>

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Best Local Similarity 100.0%; Pred. No. 1.8e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRHFPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRHFPNCPF 249

RESULT 2
JC5964
apoptosis inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Sep-2000
C:Accession: JC5964
R:Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap)
A:Reference number: JC5964; MID:98162622; PMID:9501011
A:Accession: JC5964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>
A:Cross-references: GB:U79142; NID:g2957174; PIDN:AAC39171.1; PID:g2957175
C:Superfamily: RING finger homology
F:307-351/Domain: RING finger homology <RRN>

Query Match 95.2%; Score 256; DB 2; Length 358;
Best Local Similarity 93.5%; Pred. No. 4.4e-24;
Matches 43; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: J07568
R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
Biochem. Biophys. Res. Commun. 279, 820-831, 2000
A:Title: KIAIP, a novel member of the inhibitor of apoptosis protein family.
A:Reference number: J07568; MUID: 21092523; PMID:1162435
A:Contents: Fetal Kidney
A:Accession: J07568
A:Molecule type: mRNA
A:Residues: 1-298 <LIN>
C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, plays

C:Genetics:
A:Gene: kiap
A:Map position: 20q13.3
C:Keywords: apoptosis

Query Match 47.2%; Score 127; DB 2; Length 298;
Best Local Similarity 47.8%; Pred. No. 3.5e-08;
Matches 22; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
DB 108 LAAAGFHTGHQDKVRCFCYGGLSWKRGDDPWTETHAKKFPSCQF 153

RESULT 13
A45679
Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus Cpgv
C:Species: Cydia pomonella granulosis virus Cpgv
C:Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
C:Accession: A45679
R:Crack, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A:Reference number: A45679; MUID:93188168; PMID:8445726
A:Accession: A45679
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <CRO>
A:Cross-references: GB:L05494; NID:g289583; PIDN:AA43835.1; PID:g289584
A:Note: sequence extracted from NCBI backbone (NCBI:N:127014, NCBI:P:127015)
C:Superfamily: Viral apoptosis inhibitor IAP; RING finger homology

Query Match 46.1%; Score 124; DB 2; Length 275;
Best Local Similarity 45.7%; Pred. No. 7.6e-08;
Matches 21; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
DB 129 MADAGFYTGDMTKCFYCDGLKDEPEDVPWEQHYHWFDRCAV 174

RESULT 14
T03183
probable apoptosis inhibitor - Chilo iridescent virus
C:Species: Chilo iridescent virus
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Sep-2000
C:Accession: T03183
R:Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A:Reference number: Z14834; MUID:98141693; PMID:9482589
A:Accession: T03183
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <BAH>
A:Cross-references: EMBL:AF00534; NID:g2738385; PIDN:AAB94481.1; PID:g2738454
C:Superfamily: RING finger homology
F:159-202/Domain: RING finger homology <RRN>

Query Match 43.5%; Score 117; DB 2; Length 208;

Best Local Similarity 44.0%; Pred. No. 4.3e-07;
Matches 22; Conservative 7; Mismatches 17; Indels 4; Gaps 1;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
DB 58 LSRAGFYIINIGDOVQCFYCDLKLKWKSDNPREEHKHTQDLKINCLF 107

RESULT 15
T28409
ORF MSV248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes ent
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T28409
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359.
A:Accession: T28409
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-150 <AFQ>
A:Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97724.1; PID:g4049764
C:Genetics:
A:Note: MSV248

Query Match 41.3%; Score 111; DB 2; Length 150;
Best Local Similarity 43.5%; Pred. No. 1.8e-06;
Matches 20; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
DB 37 LCEAGFYTNIGDITVCFNGLKIKNWLTYNDPWEHSHKWSFNCF 82

Search completed: May 5, 2003, 16:08:09
Job time : 7.03456 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 1.90783 Seconds

(without alignments)
1000.040 Million cell updates/sec

Title: US-08-569-749-7

Perfect score: 269
Sequence: 1 IARAGFYIIGPDVACFAC.....WAPKDDAMSEHRHFPNCPF 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269	100.0	618	BIR3_HUMAN	Q13490 homo sapien
2	264	98.1	612	BIR3_MOUSE	O62210 mus musculu
3	256	95.2	358	PIAP_PIG	O62640 sus scrofa
4	248	92.2	604	BIR2_HUMAN	Q13489 homo sapien
5	241	89.6	600	BIR2_MOUSE	O08863 mus musculu
6	192	71.4	497	BIR4_HUMAN	P98170 homo sapien
7	191	71.0	611	BIR_CRICK	O90660 gallus galli
8	187	69.5	496	BIR4_MOUSE	O60989 mus musculu
9	185	68.8	496	BIR4_RAT	O91016 rattus norv
10	155	57.6	236	BIR8_HUMAN	O96P09 homo sapien
11	155	57.6	236	BIR8_PANTR	O95M72 pan troglod
12	154	57.2	236	BIR8_GORGO	O95M71 gorilla gor
13	149	55.4	1403	BIR1_HUMAN	Q13075 homo sapien
14	141	52.4	1402	BIRG_MOUSE	O911b3 mus musculu
15	141	52.4	1403	BIRA_MOUSE	O994t5 mus musculu
16	141	52.4	1403	BIRE_MOUSE	O911b6 mus musculu
17	141	52.4	1403	BIRF_MOUSE	O24307 dtrosophila
18	140	52.0	498	IAP2_DROME	O994t4 mus musculu
19	138	51.3	1447	BIRB_MOUSE	O994t4 mus musculu
20	133.5	49.6	4829	BIR6_HUMAN	O994t9 homo sapien
21	132	49.1	268	IAP3_NPYOP	P41437 orgyia pseu
22	129	48.0	438	IAP1_DROME	O24306 dtrosophila
23	127	47.2	298	BIR7_HUMAN	O96cas5 homo sapien
24	124	46.1	275	IAP_GVCP	P47732 chillo lride
25	117	43.5	239	ZEP_IRV6	O70201 mus musculu
26	108.5	40.3	140	BIR5_MOUSE	O911b7 rattus norv
27	108.5	40.3	142	BIR5_RAT	O14064 schizosacch
28	104	38.7	997	BIR1_SCHPO	O15392 homo sapien
29	102.5	38.1	146	BIR5_HUMAN	P41435 autographa
30	96	35.7	282	IAP1_NPVAC	O10296 orgyia pseu
31	93	34.6	275	IAP1_NPYOP	P41454 autographa
32	80	29.7	249	IAP2_NPVAC	O65138 african swi
33	78.5	29.2	224	IAPL_ASFB7	

34	73.5	27.3	224	1	IAPL_ASFMI	C11452 african swi
35	72.5	27.0	224	1	IAPL_ASFCH	O11451 african swi
36	72.5	27.0	224	1	IAPL_ASFCH	O12407 african swi
37	72.5	27.0	238	1	IAPL_ASFMI	O11453 african swi
38	63.5	23.6	278	1	HUPJ_RHOCA	O03009 rhodobacter
39	58.5	21.7	284	1	CELA_ACEXY	P27897 acetobacter
40	58.5	21.7	404	1	FPRA_MERTM	Q50497 methanobact
41	57	21.2	122	1	PA21_BOTAS	P20474 bothrops as
42	56.5	21.0	181	1	VG79_HSVI1	O00148 ictaluriid h
43	56	20.8	2111	1	YB4_CAEEL	Q11107 caenorhabdi
44	55	20.4	370	1	DPSD_CRIGR	P27465 cricetus
45	54.5	20.3	424	1	EXON_NPYOP	P24081 orgyia pseu

ALIGNMENTS

RESULT 1
BIR3_HUMAN STANDARD; PRT; 618 AA.

AC Q13490; Q16516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TNFR signaling complex protein 2) (IAP homolog B).
GN BIRC3 OR API2 OR IAP2 OR MIHB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96128127; PubMed-8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TNFR signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252(1995).

[2]
RN SEQUENCE FROM N.A.
RP TISSUE-Liver;
RC MEDLINE-96149249; PubMed-8552191;
RX Liston P., Roy N., Tamai K., Lefebvre C., Balrd S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes."
RL Nature 379:349-353(1996).

[3]
RN SEQUENCE FROM N.A.
RP TISSUE-Fetal liver;
RC MEDLINE-96209843; PubMed-8643514;
RX Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).

[4]
RN SEQUENCE FROM N.A.
RP TISSUE-Uterus;
RC Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

[5]
RN STRUCTURE BY NMR OF 266-363.
RX MEDLINE-99332054; PubMed-10404221;
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat."
RL Nat. Struct. Biol. 6:648-651(1999).
-1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

```

CC CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC CC inhibit apoptotic suppressor activity.
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC CC LEUKOCYTES.
CC CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
CC CC WWW="http://www.infobiogen.fr/services/chromancer/Genes/BIRC3ID239.html"
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; L49431; AAC41942.1; -.
CC CC DR EMBL; U45879; AAC50372.1; -.
CC CC DR EMBL; U37547; AAC50508.1; -.
CC CC DR EMBL; BC016174; AAH16174.1; -.
CC CC DR PDB; 1QBH; 20-OCT-99.
CC CC DR Genew; HGNC:590; BIRC2.
CC CC DR MIM; 601721; -.
CC CC DR InterPro; IPR001370; BIR.
CC CC DR InterPro; IPR001315; CARD.
CC CC DR InterPro; IPR001841; Znf_fing.
CC CC DR Pfam; PF00097; zf-C3HC4; 1.
CC CC DR Pfam; PF00619; CARD; 1.
CC CC DR Pfam; PF00653; BIR; 3.
CC CC DR SMART; SM00238; BIR; 3.
CC CC DR SMART; SM00114; CARD; 1.
CC CC DR SMART; SM00184; RING; 1.
CC CC DR PROSITE; PS01282; BIR_REPEAT_1; 3.
CC CC DR PROSITE; PS50143; BIR_REPEAT_2; 3.
CC CC DR PROSITE; PS50209; CARD; 1.
CC CC DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC CC DR PROSITE; PS50089; ZF_RING_2; 1.
CC CC KW Apoptosis; zinc-finger; Repeat; 3D-structure.
CC CC FT REPEAT 46 113 BIR 1.
CC CC FT REPEAT 184 250 BIR 2.
CC CC FT REPEAT 269 336 BIR 3.
CC CC FT DOMAIN 453 543 CARD.
CC CC FT ZN_FING 571 606 RING-TYPE.
CC CC FT CONFLICT 157 157 S -> P (IN REF. ?).
CC CC FT CONFLICT 308 308 C -> G (IN REF. ?).
CC CC FT CONFLICT 414 414 Q -> L (IN REF. ?).
CC CC FT CONFLICT 514 514 L -> W (IN REF. ?).
CC CC SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586d CRC64;

Query Match 100.0%; Score 269; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 2.5e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LARAGFYIIGDRVACFACGKLSNWEPRDDAMSEHRHFPNCPF 46
  |||
DB 204 LARAGFYIIGDRVACFACGKLSNWEPRDDAMSEHRHFPNCPF 249

RESULT 2
ID BIR3_MOUSE STANDARD; PRT; 612 AA.
AC Q62210; Q08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
  protein 2) (MIAP2) (MIAP-2).

```

GN BIRC3 ORAP12 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RL to baculoviral inhibitor of apoptosis proteins."; Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA MEDLINE=98110590; PubMed=9441758;
RX Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RL 1 and 2 genes."; Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRS35; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL; LA9433; AAC24078.1; -;
DR EMBL; U88909; AAC53532.1; -;
DR HSSP; Q13490; IOBH.
DR MGD; MGI:1197009; Birc3.
DR InterPro; IPR001370; Birc3.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; zf_RING_1; FALSE_NEG.
DR PROSITE; PS50089; zf_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
KW REPEAT 46 113
FT REPEAT 177 243 BIR 1.
FT REPEAT 262 329 BIR 2.
FT DOMAIN 447 537 BIR 3.
FT ZN_FING 565 600 CARD.
FT CONFLICT 380 380 RING-TYPE.
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

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OY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHPNCP 46
DB 197 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHPNCP 242

RESULT 3
ID PIAP_PIG STANDARD: PRT: 358 AA.
AC 062640:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative inhibitor of apoptosis.
GN PIAP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Aorta;
RX MEDLINE-98162622; PubMed-9501011;
RA Stehlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
RT protein (Iap) family member is regulated by NF-kappa B.;"
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U791A2; AAC39171.1; -.
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_rIng.
DR Pfam: PF000097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50518; zf_RING_1; FALSE_NEG.
DR PROSITE: PS50089; zf_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
KW REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT DOMAIN 193 283 CARD.
FT ZN_FING 311 346 RING-TYPE.
SQ SEQUENCE 358 AA; 40977 MM; EB2268FA9A6190A4 CRC64;

Query Match 95.2%; Score 256; DB 1; Length 358;
Best Local Similarity 93.5%; Pred. No. 6.9e-26;
Matches 43; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHPNCP 46
DB 24 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHPNCP 69

RESULT 4
BIR2_HUMAN

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ID BIR2_HUMAN STANDARD: PRT: 604 AA.
AC Q13489; Q16628; Q9UP46; Q9HC27;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (inhibitor of apoptosis
DE protein 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TNFRF signaling complex
DE BIRC2 OR API1 OR IAP1 OR MHC.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Liver;
RX MEDLINE-96128127; PubMed-8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TNFRF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.;"
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Liver;
RX MEDLINE-96149249; PubMed-8552191;
RA Farahani R., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.;"
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Fetal liver;
RX MEDLINE-96209843; PubMed-8643514;
RA Uben A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.;"
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE-Fetal liver;
RX MEDLINE-99252096; PubMed-10233894;
RA Horrevorts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, stannin, and two novel
RT genes.;"
RL Blood 93:3418-3431(1999).
RN [5]
RP SEQUENCE OF 362-441 FROM N.A.
RX MEDLINE-20519161; PubMed-11066071;
RA Beens M., Steyls A., Dierlam J., De Wolf-Peters C., Marynen P.;
RT "Structure of the MALT gene and molecular characterization of the
RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
RT B-cell lymphomas of MALT type.;"
RL Genes Chromosomes Cancer 29:281-291(2000).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TNFR1 AND TNFR2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC tissue). This translocation is found in approximately 50% of
CC cytogenetically abnormal low-grade MALT lymphoma and involves
CC MALT1 and BIRC2.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.

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CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: L49432; AAC41943.1; -
DR EMBL: U45878; AAC50371.1; -
DR EMBL: U37546; AAC50507.1; -
DR EMBL: AF070674; AAC83232.1; -
DR EMBL: AF178945; AAC09369.1; -
DR HSSP: Q13490; IOBH.
DR Genev; HGNC:591; BIRC3.
DR MIM: 601712; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; CARD; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.
KW REPEAT 29 96 BIR 1.
FT REPEAT 169 235 BIR 2.
FT REPEAT 255 322 BIR 3.
FT DOMAIN 439 529 CARD.
FT ZN_RING 557 592 CARD.
FT SITE 442 443 RING-TYPE.
FT SITE 442 443 BREAKPOINT FOR TRANSLOCATION TO FORM
FT SITE 442 443 BIRC2-MAL1.
FT CONFLICT 18 18 N -> Y (IN REF. 4).
FT CONFLICT 119 119 N -> H (IN REF. 2).
FT CONFLICT 153 153 D -> E (IN REF. 2).
FT CONFLICT 163 163 H -> P (IN REF. 2).
FT CONFLICT 165 165 A -> P (IN REF. 2).
FT CONFLICT 191 191 K -> R (IN REF. 2).
FT CONFLICT 364 364 F -> L (IN REF. 2).
FT CONFLICT 552 552 Q -> P (IN REF. 2).
SQ SEQUENCE 604 AA; 68371 MW; 8581A00BA9AAB4A7 CRC64;

Query Match 92.2%; Score 248; DB 1; Length 604;
Best Local Similarity 91.3%; Pred. No. 1.3e-24;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LARAGFYIGPDRVACFACGKLSNWEKDDAMSEHRHFPNCPF 46
Db 189 LAKAGFYIGPDRVACFACGKLSNWEKDDAMSEHRHFPNCPF 234

RESULT 5
BIR2_MOUSE STANDARD; PRT; 600 AA.
AC 008863;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 1) (MIAP1) (MIAP-1).
GN BIRC2 OR API1 OR IAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U88908; AAC53531.1; -
DR HSSP: Q13490; IOBH.
DR MGD; MGI:1197007; Birc2.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 27 94 BIR 1.
FT REPEAT 167 233 BIR 2.
FT REPEAT 253 320 BIR 3.
FT DOMAIN 436 525 CARD.
FT ZN_RING 553 588 RING-TYPE.
SQ SEQUENCE 600 AA; 67198 MW; AD7F73B6849317D1 CRC64;

Query Match 89.6%; Score 241; DB 1; Length 600;
Best Local Similarity 89.1%; Pred. No. 1e-23;
Matches 41; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LARAGFYIGPDRVACFACGKLSNWEKDDAMSEHRHFPNCPF 46
Db 187 LAKAGFYIGPDRVACFACGKLSNWEKDDAMSEHRHFPNCPF 232

RESULT 6
BIR4_HUMAN STANDARD; PRT; 497 AA.
AC P98170; Q9N014;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP-like protein) (HILP).

```

GN BIRC4 OR API3 OR IAP3 OR XIAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai R., LeFebvre C., Baird S., Chertton-Horvat G.,
RA Farahtani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353(1996).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Fetal heart;
RX MEDLINE=96256286; PubMed=8654366;
RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
RA Giffillan M.C., Shiels H., Hardwick J.M., Thompson C.B.;
RT "A conserved family of cellular genes related to the baculovirus iap
RT gene and encoding apoptosis inhibitors.";
RL EMBO J. 15:2685-2694(1996).
RN [3]
RN SEQUENCE FROM N.A.
RA Grafham D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN FUNCTION.
RX MEDLINE=97373959; PubMed=9230442;
RA Deyereaux O.L., Takahashi R., Salvesen G.S., Reed J.C.;
RT "X-linked IAP is a direct inhibitor of cell-death proteases.";
RL Nature 388:300-304(1997).
RN [5]
RN MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.
RX MEDLINE=21634829; PubMed=11604410;
RA Verhagen A.M., Silke J., Ekert P.G., Pakusch M., Kaufmann H.,
RA Connolly L.M., Day C.L., Tikoo A., Burke R., Wöbel C., Moritz R.L.,
RA Simpson R.J., Vaux D.L.;
RT "HtrA2 promotes cell death through its serine protease activity and
RT its ability to antagonize inhibitor of apoptosis proteins.";
RL J. Biol. Chem. 277:445-454(2002).
RN [6]
RN STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.
RX MEDLINE=21020961; PubMed=11140637;
RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.,
RA Herrmann J., Wu J.C., Fesik S.W.;
RT "Structural basis for binding of Smac/DIABLO to the XIAP BIR3
RT domain.";
RL Nature 408:1004-1008(2000).
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, U45880; AAC50373.1; -

DR EMBL, U32974; AAC50518.1; -
DR EMBL, AL121601; CAB95312.1; -
DR PDB, 1G3F; 10-JAN-01.
DR Genew; HGNC:592; BIRC4.
DR MIM: 300079; -
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF000097; zf-C3HC4; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat; Thiol protease inhibitor;
KW 3D-structure.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 265 330 BIR 3.
FT ZN_FING 450 485 RING-TYPE.
FT MUTAGEN 214 214 D->S: REDUCED INTERACTION WITH PRSS25.
FT MUTAGEN 314 314 E->S: DECREASED INTERACTION WITH SMAC AND
FT WITH PRSS25.
FT CONFLICT 162 162 S->C (IN REF. 1).
FT CONFLICT 423 423 Q->P (IN REF. 2).
SQ SEQUENCE 497 AA; 56684 MW; 9D394C16D45EB635 CRC64;

Query Match 71.4%; Score 192; DB 1; Length 497;
Best Local Similarity 73.9%; Pred. No. 1,9e-17;
Matches 34; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

OY 1 LARAGFYITGPDVACVACGKLSNWEKDDAMSEHRRPNCPE 46
DB 184 LASAGLYTGTGIDQVQCFCGCKLKNWPCDRAWSEHRRHPNCF 229

RESULT 7
BIR_CHICK
ID BIR_CHICK STANDARD; PRT; 611 AA.
AC 090660;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis
DE protein).
DE ITA.
GN Gallus gallus (Chicken).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=97101112; PubMed=8945639;
RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "ITRA, a vertebrate homologue of IAP that is expressed in T
RT lymphocytes.";
RL DNA Cell Biol. 15:981-988(1996).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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RT "Rattus norvegicus x-linked inhibitor of apoptosis (IAP3) mRNA.";
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
    (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRIS25; these interactions
    inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
    and -7, while the third BIR is involved in caspase-9 inhibition.
    The interactions with SMAC and PRIS25 are mediated by the second
    and third BIR domains (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AB033366; BAA85304.1; -
DR HSPB: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF000097; Zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat.
DR REPEAT 26 93 BIR 1.
DR REPEAT 163 230 BIR 2.
DR REPEAT 264 329 BIR 3.
DR ZN_FING 449 484 RING-TYPE.
DR FT SEQUENCE 456 AA; 56072 MW; E250E3C77461A469 CRC64;
SQ
Query Match 68.8%; Score 185; DB 1; Length 496;
Best Local Similarity 71.7%; Pred. NO. 1.5e-16;
Matches 33; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFNCP 46
Db 184 LASAGLYTIGIDQVQCECCGKLNWPCDRAMSEHRRHFNCP 229
RESULT 10
BIR8_HUMAN
ID BIR8_HUMAN STANDARD; PRT; 236 AA.
AC 096P09; 096RW5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
DE inhibitor of apoptosis).
GN BIRC8 OR ILP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=11597143;
RA Lagace M., Xuan J.-Y., Young S.S., McRoberts C., Maier J.,
RA Rajcan-Separovic E., Korneluk R.G.;
RT "Genomic organization of the x-linked inhibitor of apoptosis and
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RT Identification of a novel testis-specific transcript.";
RL Genomics 77:181-188(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Fratini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezoni P., Fearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SUBUNIT: Binds to caspase-9.
CC -1- TISSUE SPECIFICITY: Testis-specific in normal tissues.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: AF420440; AAL30369.1; -
DR EMBL: AF164682; AAK81892.1; -
DR Genew: HGNC:14878; BIRC8.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00063; BIR; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger.
DR REPEAT 7 70 BIR.
DR ZN_FING 189 224 RING-TYPE.
DR FT CONFLICT 196 196 Y -> H (IN REF. 2).
DR FT SEQUENCE 236 AA; 27115 MW; CB7F034B0DDFAD9D CRC64;
SQ
Query Match 57.6%; Score 155; DB 1; Length 236;
Best Local Similarity 54.3%; Pred. NO. 5.7e-13;
Matches 25; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
QY 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDDAMSEHRRHFNCP 46
Db 23 LARAGFYAIGEDKVKQCFHCGGLANWPKEDPWEQHAQWPGCKY 68
RESULT 11
BIR8_PANTR
ID BIR8_PANTR STANDARD; PRT; 236 AA.
AC 095M72;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN BIRC8 OR ILP2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Fratini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezoni P., Fearnhead H.O., Duckett C.S.;
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RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family."
RL Mol. Biol. Cell. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL; AY030052; AAK49776.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; znf_ring.
DR Pfam; PF00653; BIR; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger.
DR REPEAT 7 70 BIR.
DR ZN_FING 189 224 RING-TYPE.
DR SEQUENCE 236 AA; 27136 MW; 64CCA3A251420EDE CRC64;
SQ
Query Match 57.6%; Score 155; DB 1; Length 236;
Best Local Similarity 54.3%; Pred. No. 5.7e-13;
Matches 25; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
OY 1 LARAGFYIGPDRVACFACGKLSNWEPRKDDAMSEHRRHPNCPF 46
DB 23 LARAGFYAIGQEDKIQCFCGGGLANWKPRKEDPWEQHAHWPCCKY 68
RESULT 12
BIR8_GORGO STANDARD; PRT; 236 AA.
AC Q95M71;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2).
GN BIRC8 OR ILP2.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21286921; PubMed-11390657;
RA Richter B.W.M., Mir S.S., Elden L.J., Lewis J., Refey S.B.,
RA Fratini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzone P., Fearhead H.O., Duckett C.S.;
RA "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family."
RT Mol. Biol. Cell. 21:4292-4301(2001).
RL -1- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL; AY030053; AAK49777.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; znf_ring.
DR Pfam; PF00653; BIR; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger.
DR REPEAT 7 70 BIR.
DR ZN_FING 189 224 RING-TYPE.
DR SEQUENCE 236 AA; 27120 MW; C3A70E39EE442E4C CRC64;
SQ
Query Match 57.2%; Score 154; DB 1; Length 236;
Best Local Similarity 52.2%; Pred. No. 7.7e-13;
Matches 24; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
OY 1 LARAGFYIGPDRVACFACGKLSNWEPRKDDAMSEHRRHPNCPF 46
DB 23 LARAGFYAIGQEDKIQCFCGGGLANWKPRKEDPWEQHAHWPCCKY 68
RESULT 13
BIR1_HUMAN STANDARD; PRT; 1403 AA.
AC Q13075; Q13730; Q99796; Q75857;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis
DE inhibitory protein).
GN BIRC1 OR NAIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95112344; PubMed-7813013;
RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yaraghi Z.,
RA Farahini R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,
RA Salih M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O.,
RA de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;
RT "The gene for neuronal apoptosis inhibitory protein is partially
RT deleted in individuals with spinal muscular atrophy."
RL Cell 80:167-178(1995).
RN [2]
RP SEQUENCE FROM N.A., AND REVISIONS.
RX TISSUE-Brain;
RX MEDLINE-98163755; PubMed-9503025;
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,
RA Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,
RA Mackenzie A.E.;
RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular
RT atrophy candidate genes SMN and NAIP."
RL Genomics 48:121-127(1998).
RN [3]
RP SEQUENCE OF 386-623 FROM N.A.
RX der Steege G., Draaijers T.G., Grootscholten P.M., Osinga J.,
RA Anzevin R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,
RA Buys C.H.C.M.;
RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.
RN [4]
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RP SEQUENCE OF 222-1403 FROM N.A.
RA Jones K., Graves T., McPherson J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Balrd S., Cherton-Horvat G.,
RA Faridani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
family of IAP genes";
RL Nature 379:349-353(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
SIGNALS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY
NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN
SPINAL CORD.
CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN
INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE 1). SMAS
ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE 1
(WERDNIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE
III (WOHLFART-RUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF
ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE
CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO
PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
NEBORN.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
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CC -----
DR EMBL: U19251; AAC52045.1; -
DR EMBL: U80017; AAC52047.1; -
DR EMBL: U21913; AAA64504.1; -
DR EMBL: AC005031; AAC62261.1; -
DR HSSP: Q13490; IOBH.
DR GeneW: HGNC:7634; BIRCL.
DR MIM: 600355; -
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR. 3.
DR SMART: SMO0238; BIR. 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50837; NACHT; 1.
KW Apoptosis; Repeat.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 758 NACHT.
FT CONFLICT 222 223 PK -> YR (IN REF. 4).
FT CONFLICT 386 387 VP -> ST (IN REF. 3).
FT CONFLICT 535 535 M -> V (IN REF. 3).
FT CONFLICT 535 535 Y -> H (IN REF. 3).
FT CONFLICT 1228 1231 MISSING (IN REF. 4).
SQ SEQUENCE 1403 AA; 159613 MW; 566304C15DA5E64 CRC64;

Query Match 55.4%; Score 149; DB 1; Length 1403;
Best Local Similarity 54.3%; Pred. No. 2.1e-11;
Matches 25; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

ID BIR_MOUSE STANDARD; PRT; 1402 AA.
AC Q9JIB3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
inhibitory protein 7).
GN BIRCL OR NAIP7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array";
RL Genome Res. 10:1095-1102(2000).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
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CC -----
DR EMBL: AF242433; AAF82749.1; -
DR HSSP: Q13490; IOBH.
DR GSD: MGI:1858256; Birc1g.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR. 3.
DR SMART: SMO0238; BIR. 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1402 AA; 159662 MW; C1DFEBA359893E0D CRC64;

Query Match 52.4%; Score 141; DB 1; Length 1402;
Best Local Similarity 52.2%; Pred. No. 2.2e-10;
Matches 24; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 1 LARAFYIIGPDRVACFAAGKLSNWEKDDAMSEHRRHFPNCPF 46
DB 181 LSAAGFVFTGKRDYVQCFSCGSLGNWEEDDPWKHAHWPFCF 226

RESULT 15
BIR_MOUSE STANDARD; PRT; 1403 AA.
ID BIR_MOUSE
AC Q9JIB3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1a (Neuronal apoptosis
inhibitory protein 1).
GN BIRCL OR NAIP1 OR NAIP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yaraqni Z., Korneluk R.G., Mackenzie A.E.;

RT "Cloning and characterization of the multiple copies of the murine
RT homologue of NAIP (neuronal apoptosis inhibitory protein).";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99431676; PubMed=10501978;
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
RT functional transcripts.";
RL Mamm. Genome 10:1032-1035(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL; AF007769; AAB69223.1; -;
DR EMBL; AF135491; AAD56763.1; -;
DR EMBL; AF242432; AAF82752.1; -;
DR HSSP; Q13490; 1QBH.
DR MGD; MGI:1298223; B1rc1a.
DR InterPro; IPR001370; BIR.
DR pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 758 NACHT.
FT CONFLICT 343 343 I -> V (IN REF. 2).
FT CONFLICT 359 359 L -> Q (IN REF. 2).
FT CONFLICT 624 624 E -> K (IN REF. 2).
FT CONFLICT 1092 1092 D -> E (IN REF. 3).
FT CONFLICT 1116 1116 D -> N (IN REF. 3).
FT CONFLICT 1123 1123 G -> R (IN REF. 3).
FT CONFLICT 1129 1129 L -> H (IN REF. 1).
FT CONFLICT 1140 1140 T -> M (IN REF. 2).
FT CONFLICT 1269 1269 A -> V (IN REF. 3).
SQ SEQUENCE 1403 AA; 158692 MW; B31630259595EB67 CRC64;

Query Match 52.4%; Score 141; DB 1; Length 1403;
Best Local Similarity 52.28; Pred. No. 2.2e-10;
Matches 24; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPGDRVACFAAGCGKLSNWEKDDAMSEHRRHPNCPF 46
I: ||| : . . . | | | | | | | | | | | | : ||| :
Db 181 LSAAGFVFTGKRDVTVCFCGSGSLGNWEGDDPWKEHAKWPFPCF 226

Search completed: May 5, 2003, 16:02:45
Job time : 2.90783 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:57:12 ; Search time 11.235 Seconds

(without alignments)
843.627 Million cell updates/sec

Title: US-08-569-749-7

Sequence: 1 LARAGFYIYIGPDVACFAC.....WEPKDDAMSEHRRHFPNCPF 46

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	243	90.3	589	11	Q9SE88	Q9SE88 rattus norv
2	243	90.3	589	11	Q9OZC6	Q9OZC6 rattus norv
3	241	89.6	374	11	Q921N0	Q921N0 mus muscula
4	236	87.7	602	11	Q9SE99	Q9SE99 rattus norv
5	228	84.8	195	13	Q91A70	Q91A70 gallus gall
6	228	84.8	197	13	Q91A69	Q91A69 gallus gall
7	228	84.8	224	13	Q91A62	Q91A62 rattus norv
8	228	84.8	324	13	Q9DDN2	Q9DDN2 gallus gall
9	228	84.8	610	13	Q57319	Q57319 gallus gall
10	199	74.0	628	13	Q8UWMD2	Q8UWMD2 brachydantio
11	190	70.6	493	13	Q8UWV8	Q8UWV8 gallus gall
12	185	68.8	496	11	Q9ESF0	Q9ESF0 rattus norv
13	185	68.8	501	11	Q9EQ05	Q9EQ05 rattus norv
14	185	68.8	501	11	Q9EQ04	Q9EQ04 rattus norv
15	155	57.6	236	4	Q96RW5	Q96RW5 homo sapien
16	155	57.6	236	4	Q96P09	Q96P09 homo sapien

17	155	57.6	236	6	Q95M72	Q95M72 pan troglod
18	154	57.2	236	6	Q95M71	Q95M71 gorilla gor
19	152	56.3	405	13	Q8UWH2	Q8UWH2 brachydantio
20	149	55.4	1160	4	Q8TD24	Q8TD24 homo sapien
21	144	53.5	403	5	Q8WRD9	Q8WRD9 ochlerotatu
22	143	53.2	106	4	Q96RW6	Q96RW6 homo sapien
23	141	52.4	597	11	Q9R015	Q9R015 mus musculu
24	140	52.0	498	5	Q96U03	Q96U03 drosophila
25	139	51.7	517	11	Q8R4U8	Q8R4U8 rattus norv
26	136	50.6	402	5	Q8T621	Q8T621 aedes albop
27	133.5	49.6	4845	11	Q88738	Q88738 mus musculu
28	132.5	49.3	153	5	Q9VEM2	Q9VEM2 drosophila
29	132	49.1	346	5	Q968T8	Q968T8 bombyx mori
30	129	48.0	264	12	Q9EN27	Q9EN27 amsacta moo
31	129	48.0	438	5	Q9VUX5	Q9VUX5 drosophila
32	127	47.2	276	12	Q8QL95	Q8QL95 mamestra co
33	127	47.2	280	4	Q9HAP7	Q9HAP7 homo sapien
34	127	47.2	298	4	Q9H2A8	Q9H2A8 homo sapien
35	127	47.2	298	4	Q96CA5	Q96CA5 homo sapien
36	126	46.8	261	12	Q9QES9	Q9QES9 epiphyas po
37	126	46.8	379	5	Q9U492	Q9U492 trichoplusi
38	125	46.5	276	12	Q89744	Q89744 buzura supp
39	123	45.7	268	12	Q91F18	Q91F18 helicoverpa
40	123	45.7	268	12	Q9E232	Q9E232 helicoverpa
41	123	45.7	281	12	Q9YNL8	Q9YNL8 choristoneu
42	123	45.7	313	12	Q9J827	Q9J827 spodoptera
43	123	45.7	377	5	Q9N107	Q9N107 spodoptera
44	117	43.5	208	12	Q55770	Q55770 chilo lride
45	115.5	42.9	4904	5	Q9VH01	Q9VH01 drosophila

ALIGNMENTS

RESULT 1	Q9SE88	PRELIMINARY;	PRT;	589 AA.
ID	Q9SE88			
AC	Q9SE88			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Inhibitor of apoptosis protein 2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Holick M., Lefevre C.A., Hicks K., Korneluk R.G.;			
RT	"Cloning and Characterization of the Rat Homologs of the Inhibitor of			
RT	Apoptosis Protein 1, 2, and 3 Genes."			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
DR	EMBL; AF183431; AAG22971.1; -.			
DR	HSSP; Q13490; IOBH.			
DR	InterPro; IPR001370; BIR.			
DR	InterPro; IPR001315; CARD.			
DR	InterPro; IPR001841; znf_fing.			
DR	Pfam; PF00653; BIR; 3.			
DR	Pfam; PF00619; CARD; 1.			
DR	Pfam; PF00097; zf-C3HC4; 1.			
DR	SMART; SM00238; BIR; 3.			
DR	SMART; SM00114; CARD; 1.			
DR	SMART; SM00184; RING; 1.			
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.			
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.			
DR	PROSITE; PS50209; CARD; 1.			
KW	Zinc-finger.			
SQ	SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;			
Query Match	90.3%; Score 243; DB 11; Length 589;			
Best Local Similarity	87.0%; Pred. NO. 4.9e-23;			
Matches	40; Conservative 3; Mismatches 3; Indels 0; Gaps 0;			

OY 1 LARAGFYITGPGDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
Db 176 LAKAGFYITGPGDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 221

RESULT 2

OY02C6 PRELIMINARY; PRT: 589 AA.
AC 0902C6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Dong Z., Denton M., Gu S.M., Saikumar P., Venkatchalam M.A.;
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF190020; AAF04585.1; -.
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; Zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 589 AA; 66777 MW; E6812FEE3EA34142 CRC64;

Query Match 90.3%; Score 243; DB 11; Length 589;
Best Local Similarity 87.0%; Pred. No. 4.9e-23;
Matches 40; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 LARAGFYITGPGDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
Db 176 LAKAGFYITGPGDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 221

RESULT 3

OY02C6 PRELIMINARY; PRT: 374 AA.
AC 0921NO;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to baculoviral IAP repeat-containing 2.
GN BIRC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011338; AAH1338.1; -.
DR MGD; MGI:1197007; Birc2.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_3.

DR PROSITE; PS50143; BIR_REPEAT_2; 3.
SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 89.6%; Score 241; DB 11; Length 374;
Best Local Similarity 89.1%; Pred. No. 5.5e-23;
Matches 41; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LARAGFYITGPGDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
Db 187 LAKAGFYITGPGDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 232

RESULT 4

OY02E9 PRELIMINARY; PRT: 602 AA.
AC 09E9E9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF183430; AAG22970.1; -.
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; Zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 602 AA; 67326 MW; CC91385EAE62DE5A CRC64;

Query Match 87.7%; Score 236; DB 11; Length 602;
Best Local Similarity 84.8%; Pred. No. 4e-22;
Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 LARAGFYITGPGDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 46
Db 189 LAKAGFYITGPGDRVACFACGKLSNWEKDDAMSEHRRHFPNCPF 234

RESULT 5

OY01A70 PRELIMINARY; PRT: 195 AA.
AC 091A70;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BREED LEKHORN; TISSUE=SPLEEN;

RX	MEDLINE-21158006; PubMed-11261557;
RA	Zhou H., Liu W., Lamont S.T.;
RT	"Genetic variation among chicken lines and mammalian species in specific genes";
RL	Poult. Sci. 80:284-288(2001).
DR	EMBL; AF221082; AAF5319.1; -.
DR	HSSP; Q13490; IQBH.
DR	InterPro; IPR001370; BIR.
DR	Pfam; PF00653; BIR; 2.
DR	SMART; SM00238; BIR; 2.
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.
DR	PROSITE; PS0143; BIR_REPEAT_2; 2.
FT	NON_TER 1 1
FT	NON_TER 195 195
SQ	SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match	84.8%;	Score 228;	DB 13;	Length 195;
Best Local Similarity	80.4%;	Pred. No. 1.3e-21;		
Matches 37; Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0;

OY	1 LARAGFYIIGGDRVACFACGGKLSNWEPKDAMSEHRHFPNCPF 46
	:: :: :: :: :: :: :: :: :: :: ::
Dd	50 LAKAGLYLGTADKVACTCGGLSNWEPKDNAMSERHRHFPCPF 95

ID	Q9IA69		PRELIMINARY;	PRT;	197 AA.
AC	Q9IA69:				
DT	01-OCT-2000	(TREMBLrel. 15,	Created)		
DT	01-OCT-2000	(TREMBLrel. 15,	Last sequence update)		
DE	01-DEC-2001	(TREMBLrel. 19,	Last annotation update)		
OS	Inhibitor of apoptosis 1	(Fragment).			
OC	Gallus gallus (Chicken).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
NCBI_TaxID=9031;	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OX	Gallus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BRED FAYOMI; TISSUE=SPLEEN;				
RX	MEDLINE-21158006; PubMed-11261557;				
RA	Zhou H., Liu W., Lamont S.J.;				
RT	"Genetic variation among chicken lines and mammalian species In				
RL	Specific genes.";				
DR	Poult. Sci. 80:284-288(2001) .				
EMBL AF221083; AAF5320.1; -	HSSP; Q13490; IOBH.				
DR	InterPro; IPR001370; BIR.				
DR	pfam; PF00653; BIR; 2.				
SMART; SM00238; BIR; 2.	PROSITE; PS01282; BIR_REPEAT_1; 2.				
DR	PROSITE; PSS0143; BIR_REPEAT_2; 2.				
FT	NON_TER				
FT	NON_TER				
SO	SEQUENCE				
	197 AA; 22602 MW; D7923DABCF623E1A CRC64;				
	Query Match	84.8%; Score 228; DB 13; Length 197;			
	Best Local Similarity	80.4%; Pred. No. 1.3e-21;			
	Matches 37; Conservative	5; Mismatches 4; Indels 0; Gaps 0.			
OY	I LARAGFYIGPDVRVACFACGKLSNWEPKDAMSEHRRHPPCPF 46				
Dd	: :: :: :: ::				
	51 LAKAGLYLTADKVACTCGQLSNWEPKDNMSEHRHFPPNCPF 96				
RESULT 7					
ID	Q88642		PRELIMINARY;	PRT;	224 AA.
AC	Q88642:				
DT	01-NOV-1998	(TREMBlrel. 08,	Created)		
DT	01-NOV-1998	(TREMBlrel. 08,	Last sequence update)		
DT	01-JUN-2002	(TREMBlrel. 21,	Last annotation update)		

DE	Inhibitor of apoptosis protein (Fragment).
ON	RAP1.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX	NCBI_TaxID=10116;
RM	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-WISTAR; TISSUE-OVARY;
RA	Bradley C.K., Lareu R.R., Dharmarajan A.M.;
RT	"Cloning and characterisation of an inhibitor of apoptosis protein
RL	(IAP) in the rat corpus luteum.";
DR	Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
EMBL	AF081503; AAC32497.1; -.
HSSP	Q13490; IQBH.
InterPro	IPRO01370; BIR.
Pfam	PF00653; BIR; 3.
SMART	SMO0238; BIR; 2.
PROSITE	PS50143; BIR_REPEAT_2; 3.
NON_TER	1 1
FT	NON_TER 224 224
SEQUENCE	224 AA; 25209 MW; 213A52534D5EB56A CRC64;
Query Match	84.8%; Score 228; DB 11; Length 224;
Best Local Similarity	80.4%; Pred. No. 1.5e-21;
Matches 37; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	
QY	1 LARAGFYIIGPGDRVACFACGGKLSLNWEPKKDDAMSEHRRHFPCPF 46 : : 105 LGKAALFYITGPGDRVPCFPACGGKLSLNWEPNDLLSEHRRHFPCPF 150

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RESULT 8
Q9DDN2
ID Q9DDN2 PRELIMINARY; PRT; 324 AA.
AC Q9DDN2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS Apoptosis inhibitor ch-IAP1 (Fragment).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.K. Jr.;
RT "The apoptosis inhibitor ch-IAP1 is a direct transcriptional target of
RT v-Rel and c-Rel."
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
EMBL: AF311289; AAG42316.1; .
DR HSSP; Q13490; IQBH.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
FT NON_TER 324 324
SQ SEQUENCE 324 AA; 36567 MW; 5E2B89DDEAE3733F3 CRC64;

Query Match 84.8%; Score 228; DB 13; Length 324;
Best Local Similarity 80.4%; Pred.No.2.2e-21;
Matches 37; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 LARAGFYIIGPDDRVACFACGCKLSNNEPKDAMSEHRRHFPCPF 46
|::| |::| |::| |::| |::| |::| |::| |::| |::|
DB 196 LAKAGLYLGTADKVCACFTCGGQLSNNEPKDNAMSEHRRHFPCPF 241

RESULT 9
Q57319 PRELIMINARY; PRT; 610 AA.

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AC 057319:
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Inhibitor of apoptosis protein 1 (IAP) (inhibitor of T cell apoptosis
DE PROTEIN).
GN IAP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WHITE LEGHORN; TISSUE=EMBRYONIC FIBROBLAST;
MEDLINE=98038801; PubMed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "Ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
RT mediator of the antiapoptotic activity of the v-Rel oncoprotein.";
RL Mol. Cell. Biol. 17:7328-7341(1997).
CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CC CELLS.
CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
CC THE V-REL-TRANSFORMED CELLS.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
CC SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
CC IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC PROCESS.
CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
CC APOPTOSIS PROTEIN REPEAT).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL: AF008592; AAB88044.1; -.
DR HSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 30 97 BIR REPEAT 1.
FT REPEAT 176 242 BIR REPEAT 2.
FT REPEAT 262 329 BIR REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B44A6 CRC64;

Query Match 84.8%; Score 228; DB 13; Length 610;
Best Local Similarity 80.4%; Pred. No. 4.4e-21;
Matches 37; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFCAGKLSNMEPKDDAMSEHRRHPNCPF 46
DB 196 LAKAGLYIGTADKAVACFCGQLSNMEPKDDAMSEHRRHPNCPF 241

RESULT 10
O8UWD2 PRELIMINARY; PRT; 628 AA.
AC O8UWD2;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE IAP1.
GN IAP1.
```

```
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF442500; AL33679.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 74.0%; Score 199; DB 13; Length 628;
Best Local Similarity 69.6%; Pred. No. 2.5e-17;
Matches 32; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

OY 1 LARAGFYIIGPDRVACFCAGKLSNMEPKDDAMSEHRRHPNCPF 46
DB 207 LAKAGLYIGGDRVACFCGQLSNMEPKDDAMSEHRRHPNCPF 252

RESULT 11
O8UWF8 PRELIMINARY; PRT; 493 AA.
AC O8UWF8;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP
RT (IAP3).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF451854; AL47170.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;
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GenCore version 5.1.6-p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:50:57 ; Search time 10.8353 Seconds
(without alignments)
676.383 Million cell updates/sec

Title: US-08-569-749-5
Perfect score: 307
Sequence: 1 CELYRMSTYTPAGVPVSE.....KYKRCGGLMDNKLGDSP 55

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.101002.*

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	55	AAW13547	Human c-IAP1 repe
2	307	100.0	306	AAU02925	Angiotensin conver
3	307	100.0	618	AAW19746	Human inhibitor of
4	307	100.0	618	AAW19583	Human apoptosis in
5	307	100.0	618	AAW13545	Human c-IAP1. Hom
6	307	100.0	618	AAW69296	Human HIAP-2 prote
7	307	100.0	618	AAW33998	Human cellular inh
8	307	100.0	618	ABG65655	Human inhibitor of
9	301	98.0	55	AAW13548	Human c-IAP2 repea
10	301	98.0	604	AAW19747	Human inhibitor of

11	301	98.0	604	18	AAW19582	Human apoptosis in
12	301	98.0	604	18	AAW13546	Human c-IAP2. Hom
13	301	98.0	604	19	AAW69295	Human HIAP-1 prote
14	301	98.0	604	20	AAW52703	Human cellular inh
15	301	98.0	604	20	AAW33997	Human cellular inh
16	301	98.0	604	23	ABG65664	Human cysteine pro
17	301	98.0	1140	22	AAU97837	Human APT2-MIT chi
18	301	98.0	1141	22	AAW50694	Human APT2-MIT chi
19	291	94.8	591	18	AAW19586	Mouse inhibitor of
20	291	94.8	591	23	ABG65668	Mouse inhibitor of
21	291	94.8	612	18	AAW13555	Mouse c-IAP. Mus
22	291	94.8	612	19	AAW69299	Mouse c-IAP. Mus
23	284	92.5	600	19	AAW69298	Mouse apoptosis in
24	284	92.5	602	18	AAW19585	Mouse inhibitor of
25	284	92.5	602	23	ABG55667	Human apoptosis in
26	159	51.8	497	18	AAW19581	Human XIAP protein
27	159	51.8	497	19	AAW69294	Human X-linked inh
28	159	51.8	497	21	AAW99985	Human XIAP protein
29	159	51.8	497	21	AAW59451	Human inhibitor of
30	159	51.8	497	23	ABG65663	Mouse inhibitor of
31	153	49.8	496	18	AAW19745	Mouse apoptosis in
32	153	49.8	496	19	AAW69297	Mouse inhibitor of
33	153	49.8	496	23	ABG65666	Human inhibitor of
34	153	49.8	496	18	AAW19584	Human XIAP protein
35	153	49.8	496	17	AAW04583	Human inhibitor of
36	145	47.2	263	23	ABB09488	Human inhibitor of
37	130.5	42.5	438	22	AAW57477	Human baculovirus-
38	129	42.0	438	22	AAW48191	Drosophila melanog
39	127	41.4	438	22	AAW61858	Drosophila melanog
40	127	41.4	438	22	ABW67347	Drosophila melanog
41	127	41.4	438	22	AAW48188	Drosophila melanog
42	127	41.4	438	22	AAW48189	Drosophila melanog
43	127	41.4	438	22	AAW48190	Drosophila melanog
44	127	41.4	438	22	AAW48190	Drosophila melanog
45	127	41.4	438	22	AAW48192	Drosophila melanog

ALIGNMENTS

RESULT 1
AAW13547 standard; Protein: 55 AA.

AAW13547:
22-JUL-1997 (first entry)
Human c-IAP1 repeat 1.
IAP, inhibitor: apoptosis; RING finger domain; restinosis;
myocardial infarction; nephritis; HIV.
Homo sapiens.
WO9706182-A1.
20-FEB-1997.
06-AUG-1996; 96WO-US12860.
08-DEC-1995; 95US-0569749.
08-AUG-1995; 95US-0512946.
(TULIA-) TULARIK INC.
Goeddel DV, Rothe M.
WPI, 1997-154209/14.
Nucleic acids encoding cellular inhibitor of apoptosis proteins
useful for apoptosis regulation in cells to reduce or increase
apoptosis and for pharmacological screening

XX PS Claim 3; Page 23; 35pp; English.
XX CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
CC AAT61590/T61591) comprise a series of defined structural domain
CC repeats and/or a RING finger domain; in particular, at least two of
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
CC sequences derived from these human genes.
CC The nucleic acid is used for recombinant prodn. of human cellular
CC inhibitor of apoptosis protein which modulates apoptosis
CC regulation. The nucleic acids are useful in therapies where
CC increased cell-specific apoptosis is desired, e.g. in restenosis,
CC inflammatory disease states, myocardial infarction, glomerular
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC They can also be used in conditions requiring a reduction in
CC apoptosis.
XX CC
SQ Sequence 55 AA;

Query Match 100.0%; Score 307; DB 18; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 55
Db 1 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 55

RESULT 2
AAU02925
ID AAU02925 standard; Protein; 306 AA.
XX AC AAU02925;
XX DT 12-SEP-2001 (first entry)
XX DE Angiotensin converting enzyme (ACEV) splice variant protein #25.
XX KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.
XX KW
OS Homo sapiens.
XX PN WO200136632-A2.
XX PD 25-MAY-2001.
XX PF 17-NOV-2000; 2000WO-IL00766.
XX PR 17-NOV-1999; 99IL-0132978.
XX PR 10-DEC-1999; 99IL-0133455.
XX PA (COMP-) COMPUGEN LTD.
XX PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX DR WPI; 2001-336004/35.
XX DR N-PSDB; AAS06025.
XX PT Novel alternative splicing variants e.g. variant of angiotensin
XX PT converting enzyme (ACEV), useful in identifying candidate compounds
XX PT capable of binding to the variant and to detect anti-variant antibodies
XX PT

XX PS Claim 4; Fig 25; 519pp; English.
XX CC The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, nonaroidotic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis.
XX CC
SQ Sequence 306 AA;

Query Match 100.0%; Score 307; DB 22; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.3e-34;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 55
Db 45 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 99

RESULT 3
AAW19746
ID AAW19746 standard; Protein; 618 AA.
XX AC AAW19746;
XX DT 16-SEP-1997 (first entry)
XX DE Human inhibitor of apoptosis protein homologue MIHB.
XX KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHB;
KW degenerative disease; infectious disease; autoimmune disease;
KW cancer; therapy; diagnosis.
XX KW
OS Homo sapiens.
XX FH Key
FH FT Region Location/Qualifiers
FT 46..113
FT /label= BIR
FT 184..250
FT /label= BIR
FT 269..337
FT /label= BIR
FT 569..606
FT /label= RING_finger
XX PN WO9723501-A1.
XX PD 03-JUL-1997.
XX PF 20-DEC-1996; 96WO-AU00827.
XX PR 22-DEC-1995; 95AU-0007275.
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PI Vaux DL;
XX DR WPI; 1997-350966/32.
XX DR N-PSDB; AAT72711.
XX PT Isolated protein homologues of viral inhibitors of apoptosis - used
XX PT

PT to modulate apoptosis for treatment of degenerative, infectious or
PT autoimmune diseases and cancer
XX
PS Claim 8; Page 51-54; 136pp; English.
XX
CC Mammalian IAP homologue B (MIB) (AAW19746) is a human homologue of
CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
CC sequence was deduced from a cDNA clone (see also AAT72711) isolated
CC from a human foetal liver cDNA library using primers based on
CC human EST sequences that resembled the BIR repeats of Oryzla
CC pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also
CC AAW19745 and AAW19747-52) and their derivatives and chemical analogues
CC can be used in methods for modulating apoptosis in animal cells,
CC specifically for treatment, by inhibition, of degenerative and
CC infectious disease or, by promotion, of cancer and autoimmune
CC disease.
XX
SQ Sequence 618 AA;

Query Match 100.0%; Score 307; DB 18; Length 618;
Best Local Similarity 100.0%; Pred. No. 3e-34;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKYKFCGCGMLDNNKLGDSP 55
Db 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKYKFCGCGMLDNNKLGDSP 99

RESULT 4
AAW19583
ID AAW19583 standard; Protein; 618 AA.
XX
AC AAW19583;
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor HIAP-2.
XX
KW Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration;
KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
KW diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 46..113
FT Domain /label= BIR-1
FT Domain 184..250
FT Domain /label= BIR-2
FT Domain 269..336
FT Domain /label= BIR-3
FT Domain 560..605
FT Domain /label= Ring_zinc_finger
XX
PN WO9706255-A2.
XX
PD 20-FEB-1997.
XX
PF 05-AUG-1996; 96WO-IB01022.
XX
PR 22-DEC-1995; 95US-0576956.
PR 04-AUG-1995; 95US-0511485.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk RG, Liston P, Mackenzie AE.
XX
DR WPI; 1997-154262/14;
DR N-PSDB; AAT70838.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection

PT of susceptibility to apoptotic disease
XX
PS Claim 27; Page 75-77; 219pp; English.
XX
CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterised by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The IAP amino acid sequences were deduced from cDNA clones (AAT70837
CC and AAT70838) from a human liver library. IAP polypeptides can be
CC expressed in host cells (in vitro or in vivo) and used in methods
CC for treating diseases and disorders involving apoptosis, esp. in a
CC human diagnosed as HIV-positive or as having AIDS, a
CC neurodegenerative disease, a myelodysplastic syndrome or an
CC ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease.
XX
SQ Sequence 618 AA;

Query Match 100.0%; Score 307; DB 18; Length 618;
Best Local Similarity 100.0%; Pred. No. 3e-34;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKYKFCGCGMLDNNKLGDSP 55
Db 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKYKFCGCGMLDNNKLGDSP 99

RESULT 5
AAW13545
ID AAW13545 standard; Protein; 618 AA.
XX
AC AAW13545;
XX
DT 22-JUL-1997 (first entry)
XX
DE Human c-IAP1.
XX
KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;
KW myocardial infarction; nephritis; HIV.
XX
OS Homo sapiens.
XX
PN WO9706182-A1.
XX
PD 20-FEB-1997.
XX
PF 06-AUG-1996; 96WO-US12860.
XX
PR 08-DEC-1995; 95US-0569749.
PR 08-AUG-1995; 95US-0512946.
XX
PA (TULA-) TULARIK INC.
XX
PI Goeddel DV, Rothe M;
XX
DR WPI; 1997-154209/14.
DR N-PSDB; AAT61590.
XX
PT Nucleic acids encoding cellular inhibitor of apoptosis proteins -
PT useful for apoptosis regulation in cells to reduce or increase
PT apoptosis and for pharmacological screening
XX
PS Disclosure; Page 18-20; 35pp; English.
XX
CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
CC AAT61590/761591) comprise a series of defined structural domain
CC repeats and/or a RING finger domain; in particular, at least two of
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
CC sequences derived from these human genes.

CC The nucleic acid is used for recombinant prodn. of human cellular
CC inhibitor of apoptosis protein which modulates apoptosis
CC regulation. The nucleic acids are useful in therapies where
CC increased cell-specific apoptosis is desired, e.g. in restinosis,
CC inflammatory disease states, myocardial infarction, glomerular
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC They can also be used in conditions requiring a reduction in
CC apoptosis.
XX
SQ Sequence 618 AA;
Query Match 100.0%; Score 307; DB 18; Length 618;
Best Local Similarity 100.0%; Pred. No. 3e-34;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGCLMDNWKLGDS 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGCLMDNWKLGDS 99
RESULT 6
AAW69296 standard; Protein; 618 AA.
XX
AC AAW69296;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human HIAP-2 protein.
XX
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein.
XX
OS Homo sapiens.
XX
PN WC09835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB00781.
XX
PR 13-FEB-1997; 97US-0800929.
XX
PA (UYOT-) UNITV OTTAWA.
XX
PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
PI Tsang B;
XX
DR WPI; 1998-467164/40.
DR N-PSDB; AAV55040.
XX
PT Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations
XX
PS Disclosure; Fig 3; 147pp; English.
XX
CC This sequence is the human HIAP-2 protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.

XX
SQ Sequence 618 AA;
Query Match 100.0%; Score 307; DB 19; Length 618;
Best Local Similarity 100.0%; Pred. No. 3e-34;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGCLMDNWKLGDS 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGCLMDNWKLGDS 99
RESULT 7
AAV33998 standard; Protein; 618 AA.
XX
AC AAV33998;
XX
DT 26-NOV-1999 (first entry)
XX
DE Human cellular inhibitor of apoptosis-1 sequence.
XX
KW Cellular inhibitor of Apoptosis-1; antisense; diagnostic; therapeutic;
KW c-IAP-1; prophylaxis; infection; inflammation; tumor formation.
XX
OS Homo sapiens.
XX
PN US5958772-A.
XX
PD 28-SEP-1999;
XX
PF 03-DEC-1998; 98US-0205204.
XX
PR 03-DEC-1998; 98US-0205204.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsett LM, Ackermann EJ;
XX
DR WPI; 1999-561047/47.
DR N-PSDB; AA222143.
XX
PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-1
PT useful for e.g. diagnostics, therapeutics, and as research reagents -
XX
PS Example 13; Columns 41-46; 32pp; English.
XX
CC The invention provides antisense compounds of 8-30 nucleotides that
CC inhibit the expression of human Cellular Inhibitor of Apoptosis-1
CC (c-IAP-1). The antisense compounds may be used for diagnostics,
CC therapeutics (for modulating the expression of c-IAP-1), prophylaxis
CC (e.g. to prevent or delay infection, inflammation, or tumor formation),
CC as research reagents (e.g. to distinguish between members of a biological
CC pathway) and in kits. The present sequence represents the human cellular
CC inhibitor of apoptosis-1.
XX
SQ Sequence 618 AA;
Query Match 100.0%; Score 307; DB 20; Length 618;
Best Local Similarity 100.0%; Pred. No. 3e-34;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGCLMDNWKLGDS 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTTGVNDKVCFCGCLMDNWKLGDS 99
RESULT 8
ABG65665 standard; Protein; 618 AA.
XX
AC ABG65665;
XX

DT 26-AUG-2002 (first entry)
 XX
 DE Human inhibitor of apoptosis, HIAP2.
 XX
 KW Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PE 27-SEP-2001; 2001WO-CA01379.
 XX
 PR 28-SEP-2000; 2000US-0672717.
 XX
 PA (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneijk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 DR MPI; 2002-479562/51.
 DR N-PSDB; ABR93871.
 XX
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases -
 PS
 PS Disclosure: Fig 3; 135pp; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC protein sequence.
 CC
 SQ Sequence 618 AA;
 QY
 Query Match 100.0%; Score 307; DB 21; Length 618;
 Best Local Similarity 100.0%; Pred. No. 3e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 CELYRMSTSTFPAGVPVSRSLRAGFYTTGVNDKVCFCGGLMDNWKLDSP 55
 45 CELYRMSTSTFPAGVPVSRSLRAGFYTTGVNDKVCFCGGLMDNWKLDSP 99
 XX
 RESULT 9
 AAM13548
 ID AAM13548 standard; Protein; 55 AA.
 XX
 AC AAM13548;
 XX
 DT 22-JUL-1997 (first entry)
 XX

DE Human c-IAP2 repeat 1.
 XX
 KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;
 KW myocardial infarction; nephritis; HIV.
 XX
 OS Homo sapiens.
 XX
 PN WO9706182-A1.
 XX
 PD 20-FEB-1997.
 XX
 PE 06-AUG-1996; 96WO-US12860.
 XX
 PR 08-DEC-1995; 95US-0569749.
 PR 08-AUG-1995; 95US-0512946.
 XX
 PA (TULA-) TULARIK INC.
 XX
 PI Goeddel DV, Rothe M;
 XX
 DR MPI; 1997-154209/14.
 XX
 PT Nucleic acids encoding cellular inhibitor of apoptosis proteins -
 PT useful for apoptosis regulation in cells to reduce or increase
 PT apoptosis and for pharmacological screening
 PS
 PS Claim 3; Page 24; 35pp; English.
 XX
 CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
 CC AAT61590/761591) comprise a series of defined structural domain
 CC repeats and/or a RING finger domain; in particular, at least two of
 CC a first domain repeat (AAM13547 or AAM13548), a second domain repeat
 CC (AAM13549 or AAM13550), and a third domain repeat (AAM13551 or AAM13552)
 CC and/or a RING finger domain (AAM13553 or AAM13554), or a consensus
 CC sequences derived from these human genes.
 CC The nucleic acid is used for recombinant prodn. of human cellular
 CC inhibitor of apoptosis protein which modulates apoptosis
 CC regulation. The nucleic acids are useful in therapies where
 CC increased cell-specific apoptosis is desired, e.g. in restinosis,
 CC inflammatory disease states, myocardial infarction, glomerular
 CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
 CC They can also be used in conditions requiring a reduction in
 CC apoptosis.
 CC
 SQ Sequence 55 AA;
 QY
 Query Match 98.0%; Score 301; DB 18; Length 55;
 Best Local Similarity 98.2%; Pred. No. 1.2e-34;
 Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 1 CELYRMSTSTFPAGVPVSRSLRAGFYTTGVNDKVCFCGGLMDNWKLDSP 55
 1 CELYRMSTSTFPAGVPVSRSLRAGFYTTGVNDKVCFCGGLMDNWKRGDSP 55
 XX
 RESULT 10
 AAM19747
 ID AAM19747 standard; Protein; 604 AA.
 XX
 AC AAM19747;
 XX
 DT 16-SEP-1997 (first entry)
 XX
 DE Human inhibitor of apoptosis protein homologue MIHC.
 XX
 KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHC;
 KW degenerative disease; infectious disease; autoimmune disease;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 DT Key Location/Qualifiers
 FT 29..97
 FT

```
FT FT /label= BIR
FT Region 169..236
FT /label= BIR
FT Region 255..323
FT /label= BIR
FT Region 556..593
FT /label= RING_finger
XX
XX WO9723501-A1.
XX
XX PD 03-JUL-1997.
XX
XX PF 20-DEC-1996; 96WO-AD00827.
XX
XX PR 22-DEC-1995; 95AU-0007275.
XX
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX PI Vaux DL.
XX
XX DR WPI; 1997-350966/32.
XX N-PSDB; AAT72712.
XX
XX PT Isolated protein homologues of viral inhibitors of apoptosis - used
PT to modulate apoptosis for treatment of degenerative, infectious or
PT autoimmune diseases and cancer
XX
XX PS Claim 9; Page 58-62; 136pp; English.
XX
XX CC Mammalian IAP homologue C (MHC) (AAW19747) is a human homologue of
CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
CC sequence was deduced from a cDNA clone (see also AAT72712) isolated
CC from a human foetal liver cDNA library using primers based on
CC human EST sequences that resembled the BIR repeats of Oryza
CC pseudotsugata polyhedrosis virus IAP. IAP homologues (see also
CC AAW19745-46 and AAW19748-52) and their derivatives and chemical
CC analogues can be used in methods for modulating apoptosis in animal
CC cells, specifically for treatment, by inhibition, of degenerative
CC and infectious disease or, by promotion, of cancer and autoimmune
CC disease.
XX
XX SQ Sequence 604 AA;

Query Match 98.0%; Score 301; DB 18; Length 604;
Best Local Similarity 98.2%; Pred. No. 2e-33;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVKCFCCGMLDNWKLGDSP 55
DB 28 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVKCFCCGMLDNWKLGDSP 82

RESULT 11
AAW19582
ID AAW19582 standard; Protein; 604 AA.
XX
XX AC AAW19582;
XX
XX DT 02-SEP-1997 (first entry)
XX
XX DE Human apoptosis inhibitor HIAP-1.
XX
XX KW Apoptosis inhibitor; HIAP-1; HIV; AIDS; neurodegeneration;
KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
XX diagnosis.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Domain 29..96
XX /label= BIR-1
XX Domain 169..235
```

```
FT FT /label= BIR-2
FT Domain 255..322
FT /label= BIR-3
FT Domain 546..591
FT /label= RING_zinc_finger
XX
XX PN WO9706255-A2.
XX
XX PD 20-FEB-1997.
XX
XX PF 05-AUG-1996; 96WO-IB01022.
XX
XX PR 22-DEC-1995; 95US-0576956.
XX PR 04-AUG-1995; 95US-0511485.
XX
XX PA (UYOT-) UNIV OTTAWA.
XX
XX PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX
XX DR WPI; 1997-154262/14.
XX N-PSDB; AAT70837.
XX
XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT of susceptibility to apoptotic disease
XX
XX PS Claim 27; Page 72-74; 219pp; English.
XX
XX CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterized by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The HIRP amino acid sequences were deduced from cDNA clones (AAT70837
CC and AAT70838) from a human liver library. IAP polypeptides can be
CC expressed in host cells (in vitro or in vivo) and used in methods
CC for treating diseases and disorders involving apoptosis, esp. in a
CC human diagnosed as HIV-positive or as having AIDS, a
CC neurodegenerative disease, a myelodysplastic syndrome or an
CC ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease.
XX
XX SQ Sequence 604 AA;

Query Match 98.0%; Score 301; DB 18; Length 604;
Best Local Similarity 98.2%; Pred. No. 2e-33;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVKCFCCGMLDNWKLGDSP 55
DB 28 CELYRMSTSTFPAGVPVSESLARAGFYTGVDKVKCFCCGMLDNWKLGDSP 82

RESULT 12
AAW13546
ID AAW13546 standard; Protein; 604 AA.
XX
XX AC AAW13546;
XX
XX DT 22-JUL-1997 (first entry)
XX
XX DE Human c-IAP2.
XX
XX KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;
KW myocardial infarction; nephritis; HIV.
XX
XX OS Homo sapiens.
XX
XX PN WO9706182-A1.
XX
XX PD 20-FEB-1997.
XX
XX PF 06-AUG-1996; 96WO-US12860.
```

XX 08-DEC-1995; 95US-0569749.
PR 08-AUG-1995; 95US-0512946.
XX
PA (TULA-) TULARIK INC.
PI Goeddel DV, Rothe M;
XX
DR WPI; 1997-154209/14.
DR N-PSDB; AAT61591.
XX
PT Nucleic acids encoding cellular inhibitor of apoptosis proteins
PT useful for apoptosis regulation in cells to reduce or increase
PT apoptosis and for pharmacological screening
XX
PS Disclosure; Page 21-23; 35pp; English.
XX
CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
CC AAT61590/761591) comprise a series of defined structural domain
CC repeats and/or a RING finger domain; in particular, at least two of
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
CC sequences derived from these human genes.
CC The nucleic acid is used for recombinant prodn. of human cellular
CC inhibitor of apoptosis protein which modulates apoptosis
CC regulation. The nucleic acids are useful in therapies where
CC increased cell-specific apoptosis is desired, e.g. in restinosis,
CC inflammatory disease states, myocardial infarction, glomerular
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC They can also be used in conditions requiring a reduction in
CC apoptosis.
XX
SQ Sequence 604 AA;
Query Match 98.0%; Score 301; DB 1e; Length 604;
Best Local Similarity 98.2%; Pred. No. 2e-33;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 1 CELYRMSTSTFPAGVPVPSERSLARAGFYTGVDKVKCFCCGLMDNWKLGDSP 55
DB 28 CELYRMSTSTFPAGVPVPSERSLARAGFYTGVDKVKCFCCGLMDNWKRGDSP 82
RESULT 13
AAW69295
ID AAW69295 standard; Protein; 604 AA.
XX
AC AAW69295;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human H1AP-1 protein.
XX
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; H1AP-1 protein.
XX
OS Homo sapiens.
XX
PN WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB00781.
XX
PR 13-FEB-1997; 97US-0800929.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
PI Tsang B;
XX
DR WPI; 1998-467164/40.

DR N-PSDB; AAV55039.
XX
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations
XX
PS Disclosure; Fig 2; 147pp; English.
XX
CC This sequence is the human H1AP-1 protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.
XX
SQ Sequence 604 AA;
Query Match 98.0%; Score 301; DB 1e; Length 604;
Best Local Similarity 98.2%; Pred. No. 2e-33;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 1 CELYRMSTSTFPAGVPVPSERSLARAGFYTGVDKVKCFCCGLMDNWKLGDSP 55
DB 28 CELYRMSTSTFPAGVPVPSERSLARAGFYTGVDKVKCFCCGLMDNWKRGDSP 82
RESULT 14
AAV52703
ID AAV52703 standard; Protein; 604 AA.
XX
AC AAV52703;
XX
DT 26-JAN-2000 (first entry)
XX
DE Human cellular inhibitor of apoptosis-2 protein.
XX
KW Identification; genetic target; gene modulation; human;
KW antisense oligonucleotide; phosphorothioate; target validation;
KW nucleotide sequence-based technology; antisense drug discovery.
XX
OS Homo sapiens.
XX
PN WO9953101-A1.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99WO-US08268.
XX
PR 13-APR-1998; 98US-0081483.
XX
PR 28-APR-1998; 98US-0067638.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowseert LM, Baker BF, McNeill J, Freiler SM, Sasmor HM, Brooks DG;
PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
XX
DR WPI; 1999-620446/53.
DR N-PSDB; AA241005.
XX
XX Identifying compounds which modulate expression of nucleic acids, used
PT to provide compounds having defined physical, chemical or bioactive
PT properties, e.g. antisense activity

PS Example 20; Page 197-202; 264pp; English.

CC A method has been developed of defining a set of compounds that modulate
CC the expression of a target nucleic acid (tNA) sequence via binding of
CC the compounds with the tNA sequence. The method comprises generating a
CC library of virtual compounds in silico according to defined criteria,
CC and evaluating in silico the binding of the virtual compounds with the
CC tNA according to defined criteria. Also described are: (1) a method of
CC defining a set of oligonucleotides (ONS) that modulate the expression of
CC a tNA sequence via binding of the ONS with the tNA sequence comprising:
CC generating a library of virtual compounds in silico according to defined
CC criteria, and evaluating in silico the binding of the virtual ONS with
CC the tNA according to defined criteria; and (2) a method of defining a
CC set of compounds that modulate the expression of a tNA sequence via
CC binding of the compounds with the tNA. The methods can be used for the
CC generation and identification of synthetic compounds having defined
CC physical, chemical or bioactive properties. Information gathered from
CC assays of such compounds is used to identify nucleic acid sequences that
CC are tractable to a variety of nucleotide sequence-based technologies,
CC e.g., antisense drug discovery and target validation. AA40852 to
CC AA41220, and AA52701 to AA52706, represent sequences used in the
CC exemplification of the present invention.

SQ Sequence 604 AA;

Query Match 98.0%; Score 301; DB 20; Length 604;
Best Local Similarity 98.2%; Pred. No. 2e-33;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDP 55
|||||
DB 28 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKRGDP 82

RESULT 15

AA33997
ID AAY33997 standard; Protein: 604 AA.

AA33997;
AC
XX
XX
DT 26-NOV-1999 (first entry)

XX Human cellular inhibitor of apoptosis-2 sequence.

DE
XX
XX
KW Cellular inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;
KW c-IAP-2; prophylaxis; infection; inflammation; tumor formation.

OS Homo sapiens.

XX
XX
PN US5958771-A.

XX
XX
PD 28-SEP-1999.

XX
XX
PF 03-DEC-1998; 98US-0205144.

XX
XX
PR 03-DEC-1998; 98US-0205144.

XX
XX
PA (ISIS-) ISIS PHARM INC.

XX
XX
PI Bennett CF, Cowser LM, Ackermann EJ;

XX
XX
DR WPI; 1999-561046/47.

XX
XX
DR N-PSDB; AA222096.

XX
XX
PT Antisense compounds complementary to Cellular inhibitor of Apoptosis-2
XX useful for e.g. diagnostics, therapeutics, and as research reagents -
XX Example 13; Columns 45-50; 33pp; English.

XX
XX
PS The invention provides antisense compounds of 8-30 nucleotides that
XX inhibit the expression of human Cellular inhibitor of Apoptosis-2
XX (c-IAP-2). The antisense compounds may be used for diagnostics,
XX therapeutics (for modulating the expression of c-IAP-2), prophylaxis

CC (e.g. to prevent or delay infection, inflammation, or tumor formation),
CC as research reagents (e.g. to distinguish between members of a biological
CC pathway) and in kits. The present sequence represents the human cellular
CC inhibitor of apoptosis-2.

SQ Sequence 604 AA;

Query Match 98.0%; Score 301; DB 20; Length 604;
Best Local Similarity 98.2%; Pred. No. 2e-33;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDP 55
|||||
DB 28 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKRGDP 82

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-08-569-749-5

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Scoring table: BLOSUM62

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Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	307	100.0	306	10	US-09-778-927A-62
2	307	100.0	618	9	US-09-201-936-8
3	307	100.0	618	10	US-09-974-592-8
4	301	98.0	604	9	US-09-201-936-6
5	301	98.0	604	10	US-09-974-592-6
6	298	97.1	68	9	US-09-201-936-19
7	292	95.1	68	9	US-09-201-936-18
8	291	94.8	591	9	US-09-201-936-42
9	291	94.8	612	10	US-09-974-592-14
10	284	92.5	600	10	US-09-974-592-12
11	284	92.5	602	9	US-09-201-936-40
12	159	51.8	68	9	US-09-201-936-17
13	159	51.8	110	9	US-09-965-967-22
14	159	51.8	497	9	US-09-201-936-4
15	159	51.8	497	10	US-09-974-592-4
16	153	49.8	68	9	US-09-201-936-16
17	153	49.8	496	9	US-09-201-936-10
18	153	49.8	496	10	US-09-974-592-10
19	150	48.9	438	1	US-08-464-588-2

20	139	45.3	110	9	US-09-965-967-21	Sequence 21, Appl
21	138	45.0	68	9	US-09-201-936-27	Sequence 21, Appl
22	133	43.3	68	9	US-09-201-936-26	Sequence 26, Appl
23	132	43.0	68	9	US-09-201-936-28	Sequence 28, Appl
24	132	43.0	68	9	US-10-041-859-18	Sequence 18, Appl
25	132	43.0	172	9	US-10-041-859-12	Sequence 12, Appl
26	130	42.3	68	9	US-09-201-936-21	Sequence 21, Appl
27	128	41.7	68	9	US-09-201-936-20	Sequence 20, Appl
28	127	41.4	68	9	US-10-041-859-19	Sequence 19, Appl
29	127	41.4	109	9	US-09-965-967-30	Sequence 30, Appl
30	127	41.4	172	9	US-10-041-859-13	Sequence 13, Appl
31	125	40.7	1403	8	US-08-913-322-22	Sequence 22, Appl
32	125	40.7	1403	8	US-08-913-322-24	Sequence 24, Appl
33	120.5	39.3	67	9	US-09-201-936-22	Sequence 22, Appl
34	115	37.5	68	9	US-10-041-859-14	Sequence 14, Appl
35	115	37.5	172	9	US-10-041-859-8	Sequence 8, Appl
36	115	37.5	346	9	US-10-041-859-2	Sequence 2, Appl
37	114.5	37.3	67	9	US-09-201-936-23	Sequence 23, Appl
38	111	36.2	66	9	US-09-201-936-25	Sequence 25, Appl
39	111	36.2	66	9	US-09-201-936-25	Sequence 25, Appl
40	111	36.2	107	9	US-09-965-967-20	Sequence 20, Appl
41	111	36.2	278	9	US-09-964-899-39	Sequence 39, Appl
42	108.5	35.3	109	9	US-09-965-967-19	Sequence 19, Appl
43	107	34.9	68	9	US-10-041-859-16	Sequence 16, Appl
44	107	34.9	172	9	US-10-041-859-10	Sequence 10, Appl
45	106	34.5	68	9	US-10-041-859-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-778-927A-62
; Sequence 62, Application US/09778927A
; Patent No. US20020068342A1
GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778, 927A
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(306)
; OTHER INFORMATION: xaa - any amino acid, unknown, or other
US-09-778-927A-62
Query Match 100.0%; Score 307; DB 10; Length 306;
Best local Similarity 100.0%; Pred. No. 2.8e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CELYRMSTSTFPAGVPVSESLARAGFYTGNDKYKFCGGLMDNKLGDSP 55
DB 45 CELYRMSTSTFPAGVPVSESLARAGFYTGNDKYKFCGGLMDNKLGDSP 99
RESULT 2
US-09-201-936-8
; Sequence 8, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.

```
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-8
```

```
Query Match          100.0%; Score 307; DB 9; Length 618;
Best Local Similarity 100.0%; Pred. No. 6.2e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKICCGGLMDNWKLGDSP 55
Db 45 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKICCGGLMDNWKLGDSP 99
```

```
RESULT 3
US-09-974-592-8
; Sequence 8, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-8
```

```
Query Match          100.0%; Score 307; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 6.2e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKICCGGLMDNWKLGDSP 55
Db 45 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKICCGGLMDNWKLGDSP 99
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```
RESULT 4
US-09-201-936-6
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; Sequence 6, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-6
```

```
Query Match          98.0%; Score 301; DB 9; Length 604;
Best Local Similarity 98.2%; Pred. No. 3.9e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKICCGGLMDNWKLGDSP 55
Db 28 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKICCGGLMDNWKRGDSP 82
```

```
RESULT 5
US-09-974-592-6
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-6
```

```
Query Match          98.0%; Score 301; DB 10; Length 604;
Best Local Similarity 98.2%; Pred. No. 3.9e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKICCGGLMDNWKLGDSP 55
Db 28 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKICCGGLMDNWKRGDSP 82
```

```
RESULT 6
US-09-201-936-19
: Sequence 19, Application US/09201936
: Publication No. US20020187946A1
: GENERAL INFORMATION:
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mackenzie, Alexander E.
: APPLICANT: Baird, Stephen
: APPLICANT: Liston, Peter
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
: FILE REFERENCE: 07891/003003
: CURRENT APPLICATION NUMBER: US/09/201,936
: EARLIER FILING DATE: 1998-12-01
: EARLIER APPLICATION NUMBER: PCT/IB96/01022
: EARLIER FILING DATE: 1996-08-05
: EARLIER APPLICATION NUMBER: 08/576,956
: EARLIER FILING DATE: 1995-12-22
: EARLIER APPLICATION NUMBER: 08/511,485
: EARLIER FILING DATE: 1995-08-04
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 19
: LENGTH: 68
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-201-936-19

Query Match          97.1%; Score 298; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 8.2e-33;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ELYRSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 55
DB 1 ELYRSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 54

RESULT 7
US-09-201-936-18
: Sequence 18, Application US/09201936
: Publication No. US20020187946A1
: GENERAL INFORMATION:
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mackenzie, Alexander E.
: APPLICANT: Baird, Stephen
: APPLICANT: Liston, Peter
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
: FILE REFERENCE: 07891/003003
: CURRENT APPLICATION NUMBER: US/09/201,936
: EARLIER FILING DATE: 1998-12-01
: EARLIER APPLICATION NUMBER: 09/011,356
: EARLIER FILING DATE: 1996-02-04
: EARLIER APPLICATION NUMBER: PCT/IB96/01022
: EARLIER FILING DATE: 1996-08-05
: EARLIER APPLICATION NUMBER: 08/576,956
: EARLIER FILING DATE: 1995-12-22
: EARLIER APPLICATION NUMBER: 08/511,485
: EARLIER FILING DATE: 1995-08-04
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 18
: LENGTH: 68
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-201-936-18

Query Match          95.1%; Score 292; DB 9; Length 68;
Best Local Similarity 98.1%; Pred. No. 5.2e-32;
```

```
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ELYRSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 55
DB 1 ELYRSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 54

RESULT 8
US-09-201-936-42
: Sequence 42, Application US/09201936
: Publication No. US20020187946A1
: GENERAL INFORMATION:
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mackenzie, Alexander E.
: APPLICANT: Baird, Stephen
: APPLICANT: Liston, Peter
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
: FILE REFERENCE: 07891/003003
: CURRENT APPLICATION NUMBER: US/09/201,936
: EARLIER FILING DATE: 1998-12-01
: EARLIER APPLICATION NUMBER: PCT/IB96/01022
: EARLIER FILING DATE: 1996-08-05
: EARLIER APPLICATION NUMBER: 08/576,956
: EARLIER FILING DATE: 1995-12-22
: EARLIER APPLICATION NUMBER: 08/511,485
: EARLIER FILING DATE: 1995-08-04
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 42
: LENGTH: 591
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-201-936-42

Query Match          94.8%; Score 291; DB 9; Length 591;
Best Local Similarity 94.5%; Pred. No. 8.3e-31;
Matches 52; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CELYRSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKLGDSP 55
DB 24 CELYRSTYSAFPGVPVSESLARAGFYTTGVNDKVCFCGGLMDNWKGDSP 78

RESULT 9
US-09-974-592-14
: Sequence 14, Application US/09974592
: Patent No. US20020120121A1
: GENERAL INFORMATION:
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mackenzie, Alexander E.
: APPLICANT: Liston, Peter
: APPLICANT: Baird, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Christine
: TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
: TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
: FILE REFERENCE: 07891/009004
: CURRENT APPLICATION NUMBER: US/09/974,592
: EARLIER FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: US 09/617,053
: PRIOR FILING DATE: 2000-07-14
: PRIOR APPLICATION NUMBER: US 08/800,929
: PRIOR FILING DATE: 1997-02-13
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14
: LENGTH: 612
: TYPE: PRT
: ORGANISM: Mus musculus
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```

1 FILEREFERENCE: 07891/003003
2
3 CURRENT APPLICATION NUMBER: US/09/201,936
4
5 CURRENT FILING DATE: 1998-12-01
6
7 EARLIER APPLICATION NUMBER: 09/011,356
8
9 EARLIER FILING DATE: 1998-02-04
10
11 EARLIER APPLICATION NUMBER: PCT/IB96/01022
12
13 EARLIER FILING DATE: 1996-08-05
14
15 EARLIER APPLICATION NUMBER: 08/576,956
16
17 EARLIER FILING DATE: 1995-12-22
18
19 EARLIER APPLICATION NUMBER: 08/511,485
20
21 EARLIER FILING DATE: 1995-08-04
22
23 NUMBER OF SEQ ID NOS: 45
24
25 SOFTWARE: FastSeq for Windows Version 3.0

```

```

; SEQ ID NO 22
; LENGTH: 110
; TYPE: PRT

```

```
; ORGANISM: Homo sapiens
US-09-965-967-22

Query Match          51.8%; Score 159; DB 3; Length 110;
Best Local Similarity 52.8%; Pred. No. 6.5e-14;
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 2 ELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVKCFCCGIMLDNKLGDGDS 54
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 16 EFNRLKTFANPSPGSPVSASTLARAGFLYTGECDTVRCFSCHAADVDRMOYGDGDS 68

RESULT 14
US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/1B96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4

Query Match          51.8%; Score 159; DB 9; Length 497;
Best Local Similarity 52.8%; Pred. No. 3.6e-13;
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 2 ELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVKCFCCGIMLDNKLGDGDS 54
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 EFNRLKTFANPSPGSPVSASTLARAGFLYTGECDTVRCFSCHAADVDRMOYGDGDS 78

RESULT 15
US-09-974-592-4
; Sequence 4, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-4

Query Match          51.8%; Score 159; DB 10; Length 497;
Best Local Similarity 52.8%; Pred. No. 3.6e-13;
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 2 ELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVKCFCCGIMLDNKLGDGDS 54
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 EFNRLKTFANPSPGSPVSASTLARAGFLYTGECDTVRCFSCHAADVDRMOYGDGDS 78

Search completed: May 5, 2003, 16:11:04
Job time : 7.77995 secs
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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003; 15:58:42 ; Search time 6.01959 Seconds

(without alignments)
878.365 Million cell updates/sec

Title: US-08-569-749-5

Perfect score: 307

Sequence: 1 CELYRMSTYTFPAGVPVSE.....KVKFCGGLMDNWKLGDSP 55

Scoring table: BLOSUM62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	618	2 S68450	apoptosis inhibito
2	301	98.0	604	2 S68449	apoptosis inhibito
3	159	51.8	497	2 S69544	apoptosis inhibito
4	140	45.6	358	2 JC5964	apoptosis inhibito
5	132	43.0	268	2 T10304	inhibitor of apopt
6	132	43.0	268	2 A53989	apoptosis-inhibiti
7	125	40.7	1232	2 A55478	neuronal apoptosis
8	122	39.7	1447	2 T42628	neuronal apoptosis
9	119	38.8	208	2 T03183	probable apoptosis
10	117	38.1	298	2 JC7568	kidney inhibitor o
11	103.5	33.7	275	2 A45679	inhibitor-of-apopt
12	103	33.6	150	2 T28409	ORF MSV248 probabl
13	102	33.2	496	2 S68452	apoptosis inhibito
14	102	33.2	497	2 S69545	apoptosis inhibito
15	93	30.3	275	2 T10310	apoptosis inhibito
16	86.5	28.2	292	2 T41772	apoptosis-inhibiti
17	83.5	27.2	286	2 D36828	IAP1 orf27 - Bomby
18	82	26.7	155	2 T30489	orf13 protein - Au
19	72.5	23.6	997	2 T43523	apoptosis inhibito
20	71.5	23.3	4845	2 T31067	cutl17 protein - fi
21	65.5	21.3	234	2 T30427	BIR repeat contain
22	61	19.9	329	2 T28403	probable apoptosis
23	60	19.5	1401	2 T17452	ORF MSV242 probabl
24	60	19.5	1401	2 T30247	Werner syndrome pr
25	59.5	19.4	337	2 T27615	hypothetical prote
26	59	19.2	733	2 T04070	hypothetical prote
27	58	18.9	288	2 B72272	liron-sulfur cluste
28	57.5	18.7	616	2 A55796	ecarin precursor -
29	57	18.6	187	2 B98183	3-methyl-adenine D

30	57	18.6	187	2 F86029	3-methyladenine DN
31	57	18.6	707	2 T40070	origin recognition
32	57	18.6	1930	2 F86200	protein F12K11.17
33	56.5	18.4	433	2 AG1044	anaerobic C4-dicar
34	56	18.2	249	2 H72858	apoptosis inhibito
35	55.5	18.1	506	2 G90430	conserved hypotnet
36	55	17.9	249	2 T41814	IAP2 orf71 - Bomby
37	55	17.9	422	2 G90259	hypothetical prote
38	55	17.9	422	2 H90271	hypothetical prote
39	55	17.9	422	2 H90275	hypothetical prote
40	55	17.9	422	2 H90501	hypothetical prote
41	55	17.9	422	2 B90327	hypothetical prote
42	55	17.9	932	2 H86325	hypothetical prote
43	55	17.9	1435	2 T01075	polypeptide - hepa
44	54.5	17.8	155	2 T37471	apoptosis inhibito
45	54.5	17.8	410	2 T49266	hypothetical prote

ALIGNMENTS

RESULT 1
S68450
apoptosis inhibitor hlap-2 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68450
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <LIS>
A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:567-611/Domain: RING finger homology <RNG>

Query Match 100.0%; Score 307; DB 2; Length 618;
Best Local Similarity 100.0%; Pred. No. 2.4e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYTFPAGVPVSESLARAGFYTGVDNKKCFCCGGLMDNWKLGDSP 55
Db 45 CELYRMSTYTFPAGVPVSESLARAGFYTGVDNKKCFCCGGLMDNWKLGDSP 99

RESULT 2
S68449
apoptosis inhibitor hlap-1 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68449
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68449
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g1184316
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:553-597/Domain: RING finger homology <RNG>

Query Match 98.0%; Score 301; DB 2; Length 604;


```

A:Cross-references: GB:U19251
C:Genetics:
A:Gene: GDB:SMAe, SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: 5q12.2-5q13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prot
F:94-110/Domain: transmembrane #status predicted <TM1>
F:470-477/Region: nucleotide-binding motif A (P-loop)
F:479-496/Domain: transmembrane #status predicted <TM2>
F:476/Binding site: ATP (Lys) #status predicted
F:618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      40.78; Score 125; DB 2; Length 1232;
Best Local Similarity 40.7%; Pred. No. 1e-07;
Matches 22; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Oy 2 ELRYMSTYTFPPAGVPEVSERSLARAGFYTYGVNDKVCFCGGLMDNMKLGDSP 55
| |:::| | |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 278 EELRLDSFKMDPRESAIVGVALAKAGLFYTGIKDLYVCESSCGGCELEKMOEGDDP 331

```

RESULT 8
 T42628
 neuronal apoptosis inhibitory protein 2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
 C:Accession: T42628
 R:Yaraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.
 Mamm. Genome 10, 761-763, 1999
 A:Title: CDNA cloning and the 5' genomic organization of Nalp2, a candidate gene for murine
 A:Reference number: Z22179; MUID:99315342; PMID:10384056
 A:Accession: T42628
 A:Status: preliminary; translated from GB/EMBL/DBST
 A:Molecule type: mRNA
 A:Residues: 1-1447 <YAR>
 A:Cross-references: EMBL:AF102871; NID:g3860228; PUD:g3860229; PIDN:AAC73002.1
 C:Genetics:
 A:Gene: Nalp2

```

Query Match      39.7%; Score 122; DB 2; Length 1447;
Best Local Similarity 40.7%; Pred. No. 2.9e-07;
Matches 22; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Oy      2  ELYRMSTYTFPPAGVPVSEKSLARAGFYTYGVNDKVKCFCCGLMDNWKLGDSP 55
      |  |  |  :  :  |  :  :  :  |  |  |  |  |  |  |  :  :  |  |  |
Db      278 EELRMDTFKDMPHESFGAVEALVKAGLFYTGKRDIYQCFSCGCMKMAEDNP 331

RESULT 9
T03183
probable apoptosis inhibitor - Chilo iridescent virus
C:Species: Chilo iridescent virus
C:Date: 24-Mar-1999 #sequence_rev1ston 24-Mar-1999 #text_change 02-Sep-2000
C:Accession: T03183
R:Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.10D
A:Reference number: Z14834; MUID:98141693; PMID:9482589
A:Accession: T03183
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <BAH>
A:Cross-references: EMBL:AF003534; NID:g2738385; PIDN:AAB94481.1; PID:g2738454
C:Superfamily: RING finger homology
F:159-202/Domain: RING finger homology <RRN>

```

```
Query Match      38.8%; Score 119; DB 2; Length 208;
Best Local Similarity 39.2%; Pred. No. 1,1e-07.
Matches 20; Conservative 12; Mismatches 19; Indels 0; Gaps 0;
```

RESULT 10
JC7568
kidney inhibitor of apoptosis protein - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7568
R.Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
Blochem. Biophys. Res. Commun. 279, 820-831, 2000
A:Title: KIP, a novel member of the inhibitor of apoptosis protein family.
A:Reference number: JC7568; PMID: 11162435
A:Contents: Fetal kidney
A:Accession: JC7568
A:Molecule type: mRNA
A:Residues: 1-298 <LIN>
C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, p
C:Genetics:
A:Gene: kiap
A:Map position: 20q13.3
C:Keywords: apoptosis

```

Query Match      38.1%; Score 117; DB 2; Length 298;
Best Local Similarity 42.6%; Pred. No. 2.8e-07;
Matches 23; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY      2  EIRMYSTYSTPPAGVPVSEKSLRAGFYTYGVNDKVKCECCGLMDNWKIGDSP 55
      1  |:::|:|  |  |:::|:|  |:::|:|  |:::|:|  |
Db      87  EELRLASFYDNPPLTAETVPEPELLAAGFFHGHQDKVRCFCYCGLSQWKRGGDP 140

RESULT 11
A45679
Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C:Species: Cydia pomonella granulosis virus CpGV
C:Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
C:Accession: A45679
R:Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A:Reference number: A45679; MUID:93188168; PMID:8445726
A:Accession: A45679
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <CRO>
A:Cross-references: GB:L05494; NID:g289583; PIDN:AAA43835.1; PID:g289584
A:Note: sequence extracted from NCBI backbone (NCBIN:127014, NCSTP:127015)
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

```

```

Query Match          33.7%; Score 103.5; DB 2; Length 275;
Best Local Similarity 35.28; Pred. No. 1.4e-05;
Matches 19; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY      2  ELYRMSTYSTPAGVSEERSLARAGFYTYGVNDKVKCFCCGLMDNWKLGDSP 55
      1  |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       7  EEVRLNTEFKMPVSF-LSPETMAKNGFYTLGRSDVRCAPCKVEIRMRKEGDP 59

RESULT 12
T28409
ORF MSY248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes ent
C:Species: Melanoplus sanguinipes entomopoxvirus
C:date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T28409
R:Alfonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MID:99102612; PMID:9847359
A:Accession: T28409
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-150 <AFO>

```

A:Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97724.1; PID:g4049764
C:Genetics:
A:Note: MSV248

Query Match 33.6%; Score 103; DB 2; Length 150;
Best Local Similarity 35.3%; Pred. No. 9.2e-06;
Matches 18; Conservative 9; Mismatches 24; Indels 0; Gaps 0;

OY 5 RMSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKLGDS 55
DB 19 RINSYENWPISLFXINRLCEAGFYTNIGDIWCFNCGIKIKNWLXNDP 69

RESULT 13

568452
apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Nov-2000
C:Accession: S68452; S78528
R:Lifton, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68452
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-496 <LIS>
A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
R:Baird, S.D.
A:Reference number: S78528
submitted to the EMBL Data Library, January 1996
A:Accession: S78528
A:Molecule type: mRNA
A:Residues: 1-36, 'A', '37', 'K', '39', 'U', '41-44', 'H', '46-58', 'Q', '60-412', 'A', '414-427', 'A', '429-496 <
A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
C:Genetics:
A:Cross-references: FlyBase:FBgn0015247
C:Function:
A:Description: apoptotic suppressor
A:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:445-489/Domain: RING finger homology <RNG>

Query Match 33.2%; Score 102; DB 2; Length 496;
Best Local Similarity 34.5%; Pred. No. 3.8e-05;
Matches 19; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

OY 1 CELYRNSTYTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKLGDS 55
DB 209 CVDARLRTFTDWPISNIOPASALAGLYYQKIGDQVRCFHCNIGLRSMQKDEP 263

RESULT 14

569545
apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 06-Dec-1998 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69545
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.D. EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69545
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: EMBL:U32373; NID:g1019116; PIDN:AAC47155.1; PID:g1019117
C:Genetics:
A:Gene: ilp
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
F:446-490/Domain: RING finger homology <RRN>

Query Match 33.2%; Score 102; DB 2; Length 497;

Best Local Similarity 34.5%; Pred. No. 3.8e-05;
Matches 19; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

OY 1 CELYRNSTYTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKLGDS 55
DB 211 CVDARLRTFTDWPISNIOPASALAGLYYQKIGDQVRCFHCNIGLRSMQKDEP 265

RESULT 15

TI0310
apoptosis-inhibiting protein 1 - Orgyia pseudotsugata nuclear polyhedrosis virus
C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OPMNPV
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C:Accession: T10310
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. Virology 229, 381-399, 1997
A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedro
A:Reference number: Z17011; MUID:97271300; PMID:9126251
A:Accession: T10310
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <AHR>
A:Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59040.1; PID:g1911287
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:223-268/Domain: RING finger homology <RRN>

Query Match 30.3%; Score 93; DB 2; Length 275;
Best Local Similarity 31.4%; Pred. No. 0.00031;
Matches 16; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

OY 5 RMSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKLGDS 55
DB 129 RRATFDHWPALNALTHDIAEAGMFTMGDETRACFCDCRVADMLPGDDP 179

Search completed: May 5, 2003, 16:08:06
Job time : 8.01958 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 2.2811 Seconds

(without alignments)
1000.040 Million cell updates/sec

Title: US-08-569-749-5

Perfect score: 307
Sequence: 1 CELYRMSFYSTFPAGVPVSE.....KVACFCGLMLDNKIDSP 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	618	1	BIR3_HUMAN Q13490 homo sapien
2	301	98.0	604	1	BIR2_HUMAN Q13489 homo sapien
3	291	94.8	612	1	BIR2_MOUSE Q62210 mus musculu
4	284	92.5	600	1	BIR2_MOUSE Q08863 mus musculu
5	247	80.5	611	1	BIR_CHICK Q90660 gallus gall
6	159	51.8	497	1	BIR_HUMAN P98170 homo sapien
7	153	49.8	496	1	BIR4_MOUSE Q60989 mus musculu
8	152	49.5	496	1	BIR4_MOUSE Q90166 mus musculu
9	140	45.6	358	1	PIAP_PIG Q62640 sus scrofa
10	134	43.6	1402	1	BIR_MOUSE Q91163 mus musculu
11	134	43.6	1403	1	BIR_MOUSE Q91166 mus musculu
12	133	43.3	1403	1	BIR_MOUSE Q91166 mus musculu
13	132	43.0	268	1	IAP3_NPVOP P41437 origyia pseu
14	127	41.4	438	1	IAP1_DROME Q24306 drosophila
15	125	40.7	1403	1	BIR1_HUMAN Q13075 homo sapien
16	122	39.7	1447	1	BIR_MOUSE Q99444 mus musculu
17	119	38.8	239	1	ZFP_IRV6 P47732 chilo iride
18	117	38.1	298	1	BIR7_HUMAN Q96ca5 homo sapien
19	111	36.2	236	1	BIR6_HUMAN Q96p09 homo sapien
20	109	35.5	1403	1	BIR_MOUSE Q99wks mus musculu
21	108	35.2	236	1	BIR_PANTR Q95m72 pan troglod
22	106	34.5	236	1	BIR_GORGO Q95m71 gorilla gor
23	103.5	33.7	275	1	IAP_GVCP P41436 cydia pomon
24	102	33.2	498	1	IAP2_DROME Q24307 drosophila
25	93	30.3	275	1	IAP1_NPVOP Q10296 origyia pseu
26	83.5	27.2	266	1	IAP1_NPVAC P41435 autographa
27	75	24.4	224	1	IAPL_ASFB7 Q65138 african swi
28	73.5	23.9	142	1	BIR5_HUMAN Q15392 homo sapien
29	72.5	23.6	997	1	BIR1_SCHPO Q14064 schizosacch
30	71.5	23.3	4829	1	BIR6_HUMAN Q9n09 homo sapien
31	70.5	23.0	140	1	BIR5_MOUSE Q70201 mus musculu
32	68.5	22.3	224	1	IAPL_ASFC3 Q11451 african swi
33	68.5	22.3	224	1	IAPL_ASFC3 Q12407 african swi

34	68.5	22.3	224	1	IAPL_ASFM1 Q11452 african swi
35	68.5	22.3	238	1	IAPL_ASFM2 Q11453 african swi
36	61.5	20.0	142	1	BIR5_RAT Q9jhy7 rattus norv
37	60	19.5	1401	1	WRN_MOUSE Q09053 mus musculu
38	57	18.6	707	1	ORC1_MOUSE P54789 schizosacch
39	56	18.2	249	1	IAP2_NPVAC P41454 autographa
40	56	18.2	1432	1	WRN_HUMAN Q14191 homo sapien
41	54.5	17.8	458	1	YMW6_CAEEL P34508 caenorhabdi
42	54.5	17.8	954	1	BIR1_YEAST P47134 saccharomyc
43	54.5	17.8	1192	1	METH_MYCPR Q33259 mycobacteri
44	53.5	17.4	949	1	IF2_HELP1 Q9zm46 helicobacte
45	53.5	17.4	1025	1	HIRA_FUGRU Q42611 fugu rubrip

ALIGNMENTS

RESULT 1
BIR3_HUMAN STANDARD; PRT; 618 AA.
AC Q13490; Q16516; (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis
DE protein 2) (H1AP2) (H1AP-2) (C-IAP1) (TNFR2-TNFRF signaling complex
DE protein 2) (IAP homolog B).
GN BIRC3 OR API2 OR IAP2 OR MIBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TNFRF signaling complex contains two novel proteins related
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertton-Horvat G.,
RA Farahani R., Mclean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NLRP and a related
RL family of IAP genes.";
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)
RT repeat.";
RL Nat. Struct. Biol. 6:648-651(1999).
CC - FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC Inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- DATABASE: NAME-Atlas Genet. Cytoenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chromocancer/genes/BIRC3ID239.html".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL: L49431; AAC41942.1; -
CC EMBL: U45879; AAC50372.1; -
CC EMBL: U37547; AAC50508.1; -
CC EMBL: BC016174; AAH16174.1; -
CC PDB: 1QBH; 20-OCT-99.
CC DR Genew; HGNC:590; BIRC2.
CC MIM: 601721; -
CC DR InterPro: IPR001370; BIR.
CC DR InterPro: IPR001315; CARD.
CC DR InterPro: IPR001841; Znf_ring.
CC DR Pfam: PF00097; zf-C3HC4; 1.
CC DR Pfam: PF00653; BIR; 3.
CC DR SMART: SM00238; BIR; 3.
CC DR SMART: SM00184; RING; 1.
CC DR PROSITE: PS01282; BIR_REPEAT_1; 3.
CC DR PROSITE: PS50143; BIR_REPEAT_2; 3.
CC DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
CC DR PROSITE: PS50089; ZF_RING_2; 1.
CC KW Apoptosis; Zinc-finger; Repeat; 3D-structure.
FT REPEAT 46 113 BIR 1.
FT REPEAT 184 250 BIR 2.
FT REPEAT 269 336 BIR 3.
FT DOMAIN 453 543 CARD.
FT ZN_RING 571 606 RING-TYPE.
FT CONFLICT 157 157 S -> P (IN REF. 2).
FT CONFLICT 308 308 C -> G (IN REF. 2).
FT CONFLICT 414 414 O -> L (IN REF. 2).
FT CONFLICT 514 514 L -> W (IN REF. 2).
SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 100.0%; Score 307; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 6; 6e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTYGVNDKYKCFCCGLMDLNKLGDSP 55
Db 45 CELYRMSTYSTFPAGVPSERSLARAGFYTYGVNDKYKCFCCGLMDLNKLGDSP 99

RESULT 2
BIR2_HUMAN STANDARD; PRT; 604 AA.
AC Q13489; O16628; Q9UP46; Q9HC27;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (Inhibitor of apoptosis
protein 1) (H1AP1) (H1AP-1) (C-IAP2) (TNFR2-TRAF signaling complex

DE protein 1) (IAP homolog C).
GN BIRC2 OR API1 OR IAP1 OR MIRC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; Pubmed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96149249; Pubmed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Fetal liver;
RX MEDLINE=96209843; Pubmed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99252096; Pubmed=10233894;
RA Horrevoets A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, stannin, and two novel
RL genes.";
RL Blood 93:3418-3431(1999).
RN [5]
RP SEQUENCE OF 362-441 FROM N.A.
RX MEDLINE=20519161; Pubmed=11066071;
RA Baens M., Steyls A., Dierlam J., De Wolf-peeters C., Harynen P.;
RT "Structure of the MLT gene and molecular characterization of the
RT genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
RT B-cell lymphomas of MALT type.";
RL Genes Chromosomes Cancer 29:281-291(2000).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROOMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC tissue). This translocation is found in approximately 50% of
CC cytogenetically abnormal low-grade MALT lymphoma and involves
CC MALTI and BIRC2.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
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DR EMBL: L49432; AAC41943.1; -
DR EMBL: U45878; AAC50371.1; -
DR EMBL: U37546; AAC50507.1; -
DR EMBL: AF070674; AAC83232.1; -
DR EMBL: AF178945; AAC09369.1; -
DR HSSP: Q13490; 1QBH.
DR Genew; HGNC:591; BIRC3.
DR MIM: 601712; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS00518; ZE_RING_1; FALSE_NEG.
DR PROSITE: PS0089; ZE_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.
FT REPEAT 29 96 BIR 1.
FT REPEAT 169 235 BIR 2.
FT REPEAT 255 322 BIR 3.
FT DOMAIN 439 529 CARD.
FT ZN_RING 557 592 RING-TYPE.
FT SITE 442 443 BREAKPOINT FOR TRANSLOCATION TO FORM BIRC2-MALT1.
FT CONFLICT 18 18 N -> Y (IN REF. 4).
FT CONFLICT 119 119 D -> H (IN REF. 2).
FT CONFLICT 153 153 D -> E (IN REF. 2).
FT CONFLICT 163 163 H -> P (IN REF. 2).
FT CONFLICT 165 165 A -> P (IN REF. 2).
FT CONFLICT 191 191 K -> R (IN REF. 2).
FT CONFLICT 364 364 F -> L (IN REF. 2).
FT CONFLICT 552 552 Q -> P (IN REF. 2).
SQ SEQUENCE 604 AA; 68371 MW; 8581A0DBA9AAB4A7 CRC64;

Query Match 98.0%; Score 301; DB 1; Length 604;
Best Local Similarity 98.2%; Pred. No. 4e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMKLGDS 55
DB 28 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMKRGDSP 82

RESULT 3
BIR3_MOUSE
ID BIR3_MOUSE STANDARD; PRT; 612 AA.
AC Q62210; 008864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 2) (MIAP2) (MIAP-2).
DE protein 2) (MIAP2) (MIAP-2).
GN BIRC3 OR API2 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE-96128127; PubMed-8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Gceddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";

Cell 83:1243-1252(1995).
(2)
RN SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE-98110590; PubMed-9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein 1 and 2 genes.";
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions inhibit apoptotic suppressor activity (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL: L49433; AAC42078.1; -
DR EMBL: U88909; AAC53532.1; -
DR HSSP: Q13490; 1QBH.
DR MGD; MGI:1197009; Birc3.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS00518; ZE_RING_1; FALSE_NEG.
DR PROSITE: PS0089; ZE_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_RING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 94.8%; Score 291; DB 1; Length 612;
Best Local Similarity 94.5%; Pred. No. 8.5e-31;
Matches 52; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNMKLGDS 55
DB 45 CELYRMSTYSAFPRGVPVPSERSLARAGFYTGVDKVCFCGGLMDNMKQGDSP 99

RESULT 4
BIR2_MOUSE
ID BIR2_MOUSE STANDARD; PRT; 600 AA.
AC Q08863;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

15-JUN-2002 (Rel. 41, last annotation update)
DE Bcl-2 protein 1 (MIAPI) (MIAPI-1).
GN BIRC2 OR API1 OR IAP1.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U88908; AAC53531.1; -
DR HSSP: Q13490; IQBH.
DR MGD; MGI:1197007; Birc2.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 27 94 BIR 1.
FT REPEAT 167 233 BIR 2.
FT REPEAT 253 320 BIR 3.
FT DOMAIN 436 525 CARD.
FT ZN_FING 553 588 RING-TYPE.
SQ SEQUENCE 600 AA; 67198 MW; AD7F73E6849317D; CRC64;
Query Match 92.5%; Score 284; DB 1; Length 600;
Best Local Similarity 90.9%; Pred. No. 7e-30; Indels 0; Gaps 0;
Matches 50; Conservative 1; Mismatches 4;
OY 1 CELYRSTSTFPAGVPSERSLARAGFYTGNDKYKCFCCGLMDNWKLDSP 55
DB 26 CELYRSTSTAFPRGVPSERSLARAGFYTGANDKYKCFCCGLMDNWKQDSDP 80
RESULT 5
BIR_CHICK STANDARD; PRT; 611 AA.

090660;
DR 01-NOV-1997 (Rel. 35, Created)
DR 01-NOV-1997 (Rel. 35, last sequence update)
DR 16-OCT-2001 (Rel. 40, last annotation update)
DE Inhibitor of apoptosis protein (IAP) (inhibitor of T cell apoptosis
DE protein).
GN ITA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_Taxid=9031;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=97101112; PubMed=8945639;
RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "ITA, a vertebrate homologue of IAP that is expressed in T
RT lymphocytes."
RL DNA Cell Biol. 15:981-988(1996).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U27466; AAB48118.1; -
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; Nuclear protein.
FT REPEAT 30 97 BIR 1.
FT REPEAT 176 242 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 446 536 CARD.
FT ZN_FING 564 599 RING-TYPE.
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;
Query Match 80.5%; Score 247; DB 1; Length 611;
Best Local Similarity 81.5%; Pred. No. 5.6e-25;
Matches 44; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY 1 CELYRSTSTFPAGVPSERSLARAGFYTGNDKYKCFCCGLMDNWKLDSP 54
DB 29 CELYRSTSTFPVNVPSERSLARAGFYTGVDKYKCFSCGLVLDNMQPQDN 82
RESULT 6

BIR4_HUMAN
 ID BIR4_HUMAN STANDARD: PRT: 497 AA.
 AC P98170: Q9N014: 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP) (IAP-like protein) (HILP).
 DE BIR4 OR API3 OR IAP3 OR XIAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=96149249; PubMed=8552191;
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G., Farhan R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";
 RL Nature 379:349-353(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal heart;
 RX MEDLINE=96256286; PubMed=8654366;
 RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L., Gilfillan M.C., Shells H., Hardwick J.M., Thompson C.B.;
 RT "A conserved family of cellular genes related to the baculovirus IAP gene and encoding apoptosis inhibitors.";
 RL EMBO J. 15:2685-2694(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Graffham D.;
 RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=97373959; PubMed=9230442;
 RA Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;
 RT "X-linked IAP is a direct inhibitor of cell-death proteases.";
 RL Nature 388:300-304(1997).
 RN [5]
 RP MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.
 RX MEDLINE=21634829; PubMed=11604410;
 RA Verhaegen A.M., Silke J., Ewert P.G., Pakusch M., Kaufmann H., Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L., Simpson R.J., Vaux D.L.;
 RT "HtrA2 promotes cell death through its serine protease activity and its ability to antagonize inhibitor of apoptosis proteins.";
 RL J. Biol. Chem. 277:445-454(2002).
 RN [6]
 RP STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.
 RX MEDLINE=21020961; PubMed=1140637;
 RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T., Herrmann J., Wu J.C., Fesik S.W.;
 RT "Structural basis for binding of Smac/Diablo to the XIAP BIR3 domain.";
 RL Nature 408:1004-1008(2000).
 CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD LEUKOCYTES.
 CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SMAC and PRSS25 are mediated by the second and third BIR domains.
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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 CC -----
 DR EMBL: U45880; AAC50373.1; -
 DR EMBL: U32974; AAC50518.1; -
 DR EMBL: AL121601; CAB95312.1; -
 DR PDB: 1G3F; 10-JAN-01.
 DR Genew; HGNC:592; BIR4.
 DR MIM: 300079; -
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR Pfam; PF00653; BIR; 3.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 DR KW Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;
 DR 3D-structure.
 FT REPEAT 26 93 BIR 1.
 FT REPEAT 163 230 BIR 2.
 FT REPEAT 265 330 BIR 3.
 FT ZN_FING 450 485 RING-TYPE.
 FT MUTAGEN 214 214 D->S: REDUCED INTERACTION WITH PRSS25.
 FT MUTAGEN 314 314 E->S: DECREASED INTERACTION WITH SMAC AND WITH PRSS25.
 FT CONFLICT 162 162 S->C (IN REF. 1).
 FT CONFLICT 423 423 Q->P (IN REF. 2).
 SQ SEQUENCE 497 AA; 56684 MW; 9D394C16D45EB635 CRC64;
 QY 2 ELYRMSTYTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDWKLDLS 54
 Db 26 EFNRLKTFANFPSPSPVSASTLARAGFLYTGEDTVRCFSCHAAVDWQYQDS 78
 Query Match 51.8%; Score 159; DB 1; Length 497;
 Best Local Similarity 52.8%; Pred. No. 2e-13;
 Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
 RESULT 7
 BIR4_MOUSE
 ID BIR4_MOUSE STANDARD: PRT: 496 AA.
 AC Q60989; Q08865;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP) (IAP homolog A) (MIAP3) (MIAP-3).
 DE (IAP homolog A) (MIAP3) (MIAP-3).
 GN BIR4 OR API3 OR XIAP OR AIPA OR MIHA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
 RX MEDLINE=96209843; PubMed=8643514;
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
 RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";
 RT Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Farhan R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;


```
CC TISSUE-Aorta; PubMed=9501011.
RX MEDLINE-98162622; PubMed=9501011.
RA Stenlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U79142; AAC39171.1; -
DR HSSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS00209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT DOMAIN 193 283 CARD.
FT ZN_FING 311 346 RING-TYPE.
SQ SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;

Query Match 45.6%; Score 140; DB 1; Length 358;
Best Local Similarity 49.0%; Pred. No. 4.8e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

OY 5 RMSTVSTPAGVPSERSLARAGFYTGVDKVKCCGGLMDNWKLGDSP 55
DB 93 RKFICFNMSSIPHPEDQLASAGFYMGHSDVKCFCCDGGI.RCWESGDDP 143

RESULT 10
BIR_MOUSE
ID BIR_MOUSE STANDARD; PRT; 1402 AA.
AC 09JIB3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
DE inhibitory protein 7).
GN BIRC1G OR NAIP7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
```

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CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF242433; AAF82749.1; -
DR HSSP: Q13490; 1QBH.
DR MGD; MG1:1858256; Birc1g.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS00837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1402 AA; 159662 MW; C1DFEBA359893E0D CRC64;

Query Match 43.6%; Score 134; DB 1; Length 1402;
Best Local Similarity 46.3%; Pred. No. 1.2e-09;
Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

OY 2 ELYRSTVSTPAGVPSERSLARAGFYTGVDKVKCCGGLMDNWKLGDSP 55
DB 278 EELRDMFKDWPQSPVGEALVRAAGFYTGKDVRCFSCGGLKWAEGDDP 331

RESULT 11
BIR_MOUSE
ID BIR_MOUSE STANDARD; PRT; 1403 AA.
AC 09R016; 09R029; P81703; 009122; 009121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis
DE inhibitory protein 5).
GN BIRC1E OR NAIP5 OR NAIP-RS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99431676; PubMed=10501978;
RX Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RT "The mouse Naip gene cluster on chromosome 13 encodes several distinct
RT functional transcripts.";
RL Mamm. Genome 10:1032-1035(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Sv;
RX MEDLINE-99417674; PubMed=10486205;
RX Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
RX Kunkel L.M., Miller W., Dietrich W.F.;
RT "Comparative sequence analysis of the mouse and human Lgn1/SMA
RT interval.";
RL Genomics 60:137-151(1999).
RN [3]
RP SEQUENCE OF 82-168 FROM N.A.
RX STRAIN=129/Sv;
RX MEDLINE-97131520; PubMed=8975718;
RX Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
RX Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
```

```
RT within the Lgn1 critical interval and contains multiple copies of Naip
RT exon 5."
RL Genomics 38:405-417(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL; AF135492; AAD56764.1; -
DR EMBL; AF131205; AAD56760.1; -
DR EMBL; U66326; AAC52974.1; -
DR HSSP; Q13490; 1QBH.
DR MGD; MGI:1298220; Bircle.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
KV Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
FT CONFLICT 92 92 K -> R (IN REF. 1).
FT CONFLICT 144 144 S -> R (IN REF. 1).
FT CONFLICT 242 242 S -> G (IN REF. 2).
FT CONFLICT 472 472 T -> A (IN REF. 2).
FT CONFLICT 516 516 A -> D (IN REF. 2).
FT CONFLICT 521 521 A -> T (IN REF. 2).
FT CONFLICT 533 533 V -> A (IN REF. 2).
FT CONFLICT 538 538 S -> I (IN REF. 2).
FT CONFLICT 1092 1092 E -> D (IN REF. 2).
FT CONFLICT 1129 1129 H -> L (IN REF. 2).
FT CONFLICT 1137 1137 R -> Q (IN REF. 2).
FT CONFLICT 1242 1242 V -> I (IN REF. 2).
FT CONFLICT 1276 1276 D -> N (IN REF. 2).
SQ SEQUENCE 1403 AA; 159695 MW; B27F645043BCE42 CRC64;

Query Match 43.6%; Score 134; DB 1; Length 1403;
Best Local Similarity 46.3%; Pred. No. 1.2e-09;
Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 2 ELYRMSTYTFPAGVPSERSLARAGFYTGVDKVKFCGCGMLDNKLGSDP 55
DB 278 EELRDMFKDMPQESFVGEALVRAGFFYTGKDIVRCFSCGCGLEKWAEGDDP 331

RESULT 12
BIRF_MOUSE STANDARD; PRT; 1403 AA.
AC Q9UIB6; P81704; 009122; 009121;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Baculoviral IAP repeat-containing protein 1f (Neuronal apoptosis
DE Inhibitory protein 6).
GN BIRclF OR NAIP6 OR NAIP-RS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
```

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RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
RN [2]
RP SEQUENCE OF 82-168 FROM N.A.
RC STRAIN=129/Svt;
RX MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
RT within the Lgn1 critical interval and contains multiple copies of Naip
RT exon 5."
RL Genomics 38:405-417(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL; AF242431; AAF82751.1; -
DR HSSP; U66327; AAC52975.1; -
DR HSSP; Q13490; 1QBH.
DR MGD; MGI:1298222; Birc1f.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
KV Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1403 AA; 159823 MW; 9D4912503358C4E9 CRC64;

Query Match 43.3%; Score 133; DB 1; Length 1403;
Best Local Similarity 46.3%; Pred. No. 1.6e-09;
Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 2 ELYRMSTYTFPAGVPSERSLARAGFYTGVDKVKFCGCGMLDNKLGSDP 55
DB 278 EELRDMFKDMPQESFVGEALVRAGFFYTGKDIVRCFSCGCGLEKWAEGDDP 331

RESULT 13
IAP3_NPVOP STANDARD; PRT; 268 AA.
AC P41437;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Apoptosis inhibitor 3 (IAP-3).
GN IAP3 OR IAP.
OS Oxygia pseudotsugata multicausid polyhedrosis virus (OpMV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=164623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94187094; PubMed=8139034;
RA Birnbaum M.J., Clem R.J., Miller L.K.;
RT "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
RT encoding a polypeptide with Cys/His sequence motifs.";
RL J. Virol. 68:2521-2528(1994).
RN [2]
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RP SEQUENCE FROM N.A.
RX MEDLINE=97271300; PubMed=9126251;
RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Hatwood S.,
RA Rohmann G.F.;
RT "The sequence of the Orgyia pseudotsugata multinnucleocapsid nuclear
RL polyhedrosis virus genome."
RL Virology 229:381-399(1997).
CC -1- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY
CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: L22564; AAC02610.1; -
DR HSSP: U75930; AAC59034.1; -.
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 18 84 BIR 1.
FT REPEAT 111 178 BIR 2.
FT ZN_FING 221 256 RING-TYPE.
SQ SEQUENCE 268 AA; 30076 MW; DF89175FDE85A708 CRC64;

Query Match 43.0%; Score 132; DB 1; Length 268;
Best Local Similarity 42.6%; Pred. No. 4.1e-10;
Matches 23; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 2 ELYRSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDWKLGDSP 55
Db 111 EAARLRTFAEMPRLKORPEELAEAGFYTGVDKVCFCGGLMDWKLGDSP 164

RESULT 14
IAP1_DROME STANDARD; PRT; 438 AA.
ID IAP1_DROME
AC Q24306;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis 1 inhibitor (inhibitor of apoptosis 1) (DIAP1) (Thread
DE protein).
GN IAP1 OR TH.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX TISSUE-Eye imaginal disk;
RX MEDLINE=96128128; PubMed=8548811;
RA Hay B.A., Wassarman D.A., Rubin G.M.;
RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins
RL function to block cell death."
RL Cell 83:1253-1262(1995).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND
CC HID-DEPENDENT CELL DEATH IN THE EYE.

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CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: L49440; AAC41609.1; -
DR HSSP: Q13490; IQBH.
DR FlyBase: FBgn0003691; th.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 44 110 BIR 1.
FT REPEAT 226 293 BIR 2.
FT ZN_FING 391 426 RING-TYPE.
SQ SEQUENCE 438 AA; 48098 MW; A6C22C8EDF5AEF29 CRC64;

Query Match 41.4%; Score 127; DB 1; Length 438;
Best Local Similarity 42.6%; Pred. No. 3.1e-09;
Matches 23; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

QY 2 ELYRSTSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDWKLGDSP 55
Db 226 ETARLRTFAEMPRLKORPEELAEAGFYTGVDKVCFCGGLMDWKLGDSP 279

RESULT 15
BIR1_HUMAN STANDARD; PRT; 1403 AA.
ID BIR1_HUMAN
AC Q13075; Q13730; Q99796; O75857;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis
DE inhibitory protein).
GN BIR1 OR NAIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX TISSUE-Fetal brain;
RX MEDLINE=95112344; PubMed=7813013;
RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yaraghi Z.,
RA Farahani R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,
RA Salih M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O.,
RA de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;
RT "The gene for neuronal apoptosis inhibitory protein is partially
RL deleted in individuals with spinal muscular atrophy."
RL Cell 80:167-178(1995).
[2]
RP SEQUENCE FROM N.A. AND REVISIONS.
RX TISSUE-Brain;
RX MEDLINE=98163755; PubMed=9503025;
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,
RA Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,
RA Mackenzie A.E.;
RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular

```

RT atrophy candidate genes SMN and NAIP.";
RL Genomics 48:121-127(1998).
RL [3]
RP SEQUENCE OF 386-623 FROM N.A.
RA der Steege G., Draaflers T.G., Grootsohollen P.M., Osinga J.,
RA Anzeveno R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,
RA Buys C.H.C.M.;
RL Submitted (MAY-1995) to the EMBL/Genbank/DDbJ databases.
RL [4]
RP SEQUENCE OF 222-1403 FROM N.A.
RA Jones K., Graves T., McPherson J.;
RL Submitted (JUN-1998) to the EMBL/Genbank/DDbJ databases.
RL [5]
RP FUNCTION.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Parahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes";
RL Nature 379:349-353(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS; INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY
CC NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN
CC SPINAL CORD.
CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN
CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE I). SMAS
CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I
CC (WERDNIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE
CC III (WOLFF-PARK-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF
CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE
CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO
CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
CC NEWBORNS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL; U19251; AAC52045.1; -;
DR EMBL; U80017; AAC52047.1; -;
DR EMBL; U21913; AAA64504.1; -;
DR EMBL; AC005031; AAC62261.1; -;
DR HSSP; Q13490; IOBH.
DR Genew; HGNC:7634; BIRC1.
DR MIM; 600355; -;
DR InterPro; IPR01370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
KW Apoptosis; Repeat.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 758 NACHT.
FT CONFLICT 222 223 PK -> YR (IN REF. 1).
FT CONFLICT 386 387 VP -> ST (IN REF. 3).
FT CONFLICT 535 535 M -> V (IN REF. 3).
FT CONFLICT 553 553 Y -> H (IN REF. 3).
FT CONFLICT 1228 1231 MISSING (IN REF. 4).
SQ SEQUENCE 1403 AA; 159613 MW; 566504C154DA5E64 CRC64;

	Matches	22;	Conservative	11;	Mismatches	21;	Indels	0;	Gaps	0;
QY	2	EIYRMSYSTFPAGVPYSESLARAGFYTTGVADKVKFCGCGMLDNNKL3DSF	55	1	:	:	:	:	:	:
Db	278	EELRLDSFKDMRESAGVAAALAKAGLEFYTGINDIVGCFSCGCGLEKKNQEGDDP	331	1	:	:	:	:	:	:

Search completed: May 5, 2003, 16:02:42
Job time : 4.28111 secs

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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:57:12 ; Search time 13.4332 Seconds

(without alignments)
843.627 Million cell updates/sec

Title: US-08-569-749-5

Perfect score: 307
Sequence: 1 CELYRNSTYTFPAGVPVSE.....KVKCFCCGMLDWMKLGDPSP 55

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	97.1	602	11	Q9ESE9
2	291	94.8	589	11	Q9ESE8
3	291	94.8	589	11	Q9QZC6
4	281	91.5	374	11	Q921N0
5	247	80.5	324	13	Q9DDN2
6	247	80.5	324	13	Q9DDN2
7	191	62.2	610	13	Q57319
8	157	51.1	493	13	Q8UVF8
9	155	50.5	405	13	Q8UWH2
10	152	49.5	496	11	Q9ESF0
11	152	49.5	501	11	Q9EQ05
12	152	49.5	501	11	Q9EQ04
13	145	47.2	264	12	Q9EN27
14	143	46.6	195	13	Q91A70
15	143	46.6	197	13	Q91A69
16	140	45.6	281	12	Q9YNL8

17	136	44.3	276	12	Q8Q195
18	136	44.3	517	11	Q8RAU8
19	134	43.6	597	11	Q9R015
20	131	42.7	224	11	Q88642
21	131	42.7	243	12	Q91EW1
22	127	41.4	438	5	Q9VUX5
23	125	40.7	1160	4	Q8TDZ4
24	122	39.7	403	5	Q8WRD9
25	119	38.8	208	12	Q55770
26	117	38.1	280	4	Q9HAP7
27	117	38.1	298	4	Q9H2A8
28	117	38.1	298	4	Q96CA5
29	115	37.5	346	5	Q96878
30	115	37.5	402	5	Q8T621
31	113.5	37.0	153	5	Q9VEM2
32	111	36.2	236	4	Q96RW5
33	111	36.2	236	4	Q96P09
34	111	36.2	313	12	Q9J827
35	108	35.2	236	6	Q95M72
36	107	34.9	379	5	Q9U492
37	106	34.5	106	4	Q96RW6
38	106	34.5	236	6	Q95M71
39	106	34.5	377	5	Q9NJ07
40	105.5	34.4	276	12	Q89744
41	104	33.9	109	6	Q8WMT4
42	103	33.6	150	12	Q9YVJ4
43	103	33.6	261	12	Q90ES9
44	102	33.2	498	5	Q96003
45	101	32.9	268	12	Q9E232

ALIGNMENTS

RESULT 1	Q9ESE9	PRELIMINARY:	PRT:	602 AA.
ID	Q9ESE9			
AC	Q9ESE9			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2002 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Inhibitor of apoptosis protein 1.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.,			
RT	"Cloning and Characterization of the Rat Homologs of the Inhibitor of			
RT	Apoptosis Protein 1, 2, and 3 Genes."			
RL	Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.			
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
DR	EMBL; AF163430; AAC22970.1; ..			
DR	HSSP; Q13490; IOBH.			
DR	InterPro; IPR001370; BIR.			
DR	InterPro; IPR001315; CARD.			
DR	InterPro; IPR001841; znf_ring.			
DR	Pfam; PF00653; BIR; 3.			
DR	Pfam; PF00619; CARD; 1.			
DR	Pfam; PF00097; zf-C3HC4; 1.			
DR	SMART; SM00238; BIR; 3.			
DR	SMART; SM00114; CARD; 1.			
DR	SMART; SM00184; RING; 1.			
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.			
DR	PROSITE; PS0143; BIR_REPEAT_2; 3.			
DR	PROSITE; PS50209; CARD; 1.			
KW	zinc-finger.			
SQ	SEQUENCE 602 AA; 67326 MW; CC91385EEA62DE5A CRC64;			
Query Match	97.1%;	Score 298;	DB 11;	Length 602;
Best Local Similarity	96.4%;	Pred. No. 1.2e-31;		
Matches	53;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

Q8Q195 mamestra co
Q8RAU8 rattus norv
Q9R015 mus musculu
Q88642 rattus norv
Q91EW1 cydia pomon
Q9VUX5 drosophila
Q8TDZ4 homo sapien
Q8WRD9 ochlerotatu
Q55770 chilio iride
Q9HAP7 homo sapien
Q9H2A8 homo sapien
Q96CA5 homo sapien
Q96878 bombyx mori
Q8T621 aedes albop
Q9VEM2 drosophila
Q96RW5 homo sapien
Q96P09 homo sapien
Q9J827 spodoptera
Q95M72 pan troglod
Q9U492 trichoplusi
Q96RW6 homo sapien
Q95M71 gorilla gor
Q9NJ07 spodoptera
Q89744 buzzara supp
Q8WMT4 bos taurus
Q9YVJ4 melanoplus
Q90ES9 epiphyas po
Q96003 drosophila
Q9E232 helioverpa

DR InterPro; IPR001370; BIR.

RP SEQUENCE FROM N.A.
RN [1]

RP SEQUENCE FROM N.A.
RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;

DR PROSITH

DT 01-MAR

DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT *Identification of chicken inhibitor of apoptosis protein XIAP
RT (IAP3)."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF451854; AL447170.1; -.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB611BC CRC64;
Query Match 51.1%; Score 157; DB 13; Length 493;
Best Local Similarity 54.7%; Pred. No. 1.1e-12;
Matches 29; Conservative 7; Mismatches 17; Indels 0; Gaps 0;
QY 2 ELYRMSTYTFPAGVPVSESLARAGFYTGVDKVKCFCCGLMDNMKLGDS 54
ID 08UWH2 PRELIMINARY; PRT; 405 AA.
AC 08UWH2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Xiap.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF439767; AL32047.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 405 AA; 45564 MW; A366E342D83BECAB CRC64;
Query Match 50.5%; Score 155; DB 13; Length 405;
Best Local Similarity 51.0%; Pred. No. 1.6e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 5 RMSTYTFPAGVPVSESLARAGFYTGVDKVKCFCCGLMDNMKLGDS 55
ID 140 RLSIFNMNPPADSVRPEDLAEGMYIGIDNVQCRCGGSLSGMEGGDDP 190

RESULT 10

ID 09ESF0 PRELIMINARY; PRT; 496 AA.

AC 09ESF0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF183429; AAG22969.1; -.
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
KW Zinc-finger.

SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;

Query Match 49.5%; Score 152; DB 11; Length 496;
Best Local Similarity 50.9%; Pred. No. 5e-12;
Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 2 ELYRMSTYTFPAGVPVSESLARAGFYTGVDKVKCFCCGLMDNMKLGDS 54
ID 26 EFRRLKTRANFPSSPVASASTLARAGLTYTGEGDTVQCFSCHAAVDRWQYDGS 78

RESULT 11

ID 09EQ05 PRELIMINARY; PRT; 501 AA.

AC 09EQ05;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=OVARY;
RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
RT protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF304333; AAG41192.1; -.
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR SMART; SM00238; BIR; 3.

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 3.26267 Seconds

(without alignments)
432.866 Million cell updates/sec

Title: US-08-569-749-9

Perfect score: 295
Sequence: 1 PEOLASAGFYVGRNDVYK.....CWESGDDPWVEHAKWFPFCE 48

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgcn2_6/ptodata/1/1aa/6A_COMB.pap:*
4: /cgcn2_6/ptodata/1/1aa/6B_COMB.pap:*
5: /cgcn2_6/ptodata/1/1aa/PCTUS_COMB.pap:*
6: /cgcn2_6/ptodata/1/1aa/Backfile1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	295	100.0	48	4	US-08-569-749-9
2	295	100.0	48	5	PCT-US96-12860-9
3	295	100.0	438	5	PCT-US95-05922A-2
4	295	100.0	618	4	US-08-569-749-2
5	295	100.0	618	4	US-09-069-023-29
6	295	100.0	618	5	PCT-US96-12860-2
7	283	95.9	68	2	US-08-511-485-27
8	283	95.9	618	2	US-08-511-485-8
9	283	95.9	618	3	US-09-212-971-8
10	283	95.9	618	4	US-08-800-929A-8
11	283	95.9	618	4	US-09-617-053A-8
12	282	95.6	48	4	US-08-569-749-10
13	282	95.6	48	5	PCT-US96-12860-10
14	282	95.6	68	2	US-08-511-485-26
15	282	95.6	604	2	US-08-511-485-6
16	282	95.6	604	3	US-09-212-971-6
17	282	95.6	604	4	US-08-800-929A-6
18	282	95.6	604	4	US-08-569-749-4
19	282	95.6	604	4	US-09-617-053A-6
20	282	95.6	604	5	PCT-US96-12860-4
21	282	95.6	612	3	US-09-212-971-14
22	282	95.6	612	4	US-08-800-929A-14
23	282	95.6	612	4	US-08-569-749-14
24	282	95.6	612	4	US-09-617-053A-14
25	282	95.6	612	5	PCT-US96-12860-14
26	268	90.8	600	3	US-09-212-971-12
27	268	90.8	600	4	US-08-800-929A-12

28	268	90.8	600	4	US-09-617-053A-12	Sequence 12, Appl
29	231	78.3	50	4	US-08-975-080-31	Sequence 31, Appl
30	230	78.0	50	4	US-08-975-080-22	Sequence 22, Appl
31	230	78.0	50	4	US-08-975-080-30	Sequence 30, Appl
32	198	67.1	68	2	US-08-511-485-28	Sequence 28, Appl
33	198	67.1	268	3	US-08-836-134-22	Sequence 22, Appl
34	198	67.1	268	4	US-09-493-784-22	Sequence 22, Appl
35	187	63.4	50	4	US-08-975-080-21	Sequence 21, Appl
36	182	61.7	68	2	US-08-511-485-29	Sequence 29, Appl
37	182	61.7	275	3	US-08-511-485-12	Sequence 12, Appl
38	182	61.7	275	3	US-08-836-134-21	Sequence 21, Appl
39	182	61.7	275	4	US-09-493-784-21	Sequence 21, Appl
40	178	60.3	1151	4	US-08-836-134-23	Sequence 23, Appl
41	178	60.3	1151	4	US-09-493-784-23	Sequence 23, Appl
42	178	60.3	1232	3	US-08-836-134-2	Sequence 2, Appl
43	178	60.3	1232	4	US-09-493-784-2	Sequence 2, Appl
44	174	59.0	66	2	US-08-511-485-25	Sequence 25, Appl
45	174	59.0	236	4	US-09-239-867-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-569-749-9
; Sequence 9, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: DAVID V
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,749
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-569-749-9

Query Match 100.0%; Score 295; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.7e-30;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKFCDCDGLRCWESGDDPWVEHAKWFPFCE 48
DB 1 PEOLASAGFYVGRNDVYKFCDCDGLRCWESGDDPWVEHAKWFPFCE 48

RESULT 2
PCT-US96-12860-9
; Sequence 9, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12860-9

Query Match 100.0%; Score 295; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.7e-30;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQLASAGFYVGRNDVKCCDGLRCWESGDDPWVEHAKWPRCE 48
|||||
DB 1 PQLASAGFYVGRNDVKCCDGLRCWESGDDPWVEHAKWPRCE 48

RESULT 3
PCT-US95-05922A-2
; Sequence 2, Application PC/TUS9505922A
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05922A

FILING DATE: 11 MAY 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-292
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-05922A-2

Query Match 100.0%; Score 295; DB 5; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.1e-29;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQLASAGFYVGRNDVKCCDGLRCWESGDDPWVEHAKWPRCE 48
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DB 107 PQLASAGFYVGRNDVKCCDGLRCWESGDDPWVEHAKWPRCE 154

RESULT 4
US-08-569-749-2
; Sequence 2, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,749
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-569-749-2

Query Match 100.0%; Score 295; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 6e-29;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVYKFCDCDGLRCWESGDDPWVEHAKWFPCE 48
|||||
Db 287 PEOLASAGFYVGRNDVYKFCDCDGLRCWESGDDPWVEHAKWFPCE 334

RESULT 5
US-09-069-023-29
Sequence 29, Application US/09069023A
Patent No. 6348573
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
FILE REFERENCE: UM-03333
CURRENT FILING DATE: 1998-04-27
CURRENT APPLICATION NUMBER: US/09/069,023A
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-069-023-29

Query Match 100.0%; Score 295; DB 4; Length 618;
Best Local Similarity 100.0%; Pred. No. 6e-29;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVYKFCDCDGLRCWESGDDPWVEHAKWFPCE 48
|||||
Db 287 PEOLASAGFYVGRNDVYKFCDCDGLRCWESGDDPWVEHAKWFPCE 334

RESULT 6
PCT-US96-12860-2
Sequence 2, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749 -
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-2

Query Match 100.0%; Score 295; DB 5; Length 618;
Best Local Similarity 100.0%; Pred. No. 6e-29;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVYKFCDCDGLRCWESGDDPWVEHAKWFPCE 48
|||||
Db 287 PEOLASAGFYVGRNDVYKFCDCDGLRCWESGDDPWVEHAKWFPCE 334

RESULT 7
US-08-511-485-27
Sequence 27, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-27

Query Match 95.9%; Score 283; DB 2; Length 68;
Best Local Similarity 97.9%; Pred. No. 1.7e-28;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVYKFCDCDGLRCWESGDDPWVEHAKWFPCE 48
|||||
Db 19 PEOLASAGFYVGRNDVYKFCDCDGLRCWESGDDPWVEHAKWFPCE 66

RESULT 8
US-08-511-485-8
Sequence 8, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-8

Query Match 95.9%; Score 283; DB 2; Length 618;
Best Local Similarity 97.9%; Pred. No. 1.9e-27;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHWPCE 48
Db 287 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHWPCE 334

RESULT 9
US-09-212-971-8
Sequence 8, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
EARLIER FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-8

Query Match 95.9%; Score 283; DB 3; Length 618;
Best Local Similarity 97.9%; Pred. No. 1.9e-27;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHWPCE 48
Db 287 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHWPCE 334

RESULT 10
US-08-800-929A-8
Sequence 8, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-8

Query Match 95.9%; Score 283; DB 4; Length 618;
Best Local Similarity 97.9%; Pred. No. 1.9e-27;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHWPCE 48

Db 287 PEOLASAGFYVGRNDVYKFCGCDGGLRCWESGDDPWVEHAKWPFRC 334

RESULT 11

US-09-617-053A-8

Sequence 8, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-617-053A-8

Query Match 95.9%; Score 283; DB 4; Length 618;
Best Local Similarity 97.9%; Pred. No. 1.9e-27;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVYKFCGCDGGLRCWESGDDPWVEHAKWPFRC 48
Db 287 PEOLASAGFYVGRNDVYKFCGCDGGLRCWESGDDPWVEHAKWPFRC 334

RESULT 12

US-08-569-749-10

Sequence 10, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-10

Query Match 95.6%; Score 282; DB 4; Length 48;
Best Local Similarity 93.8%; Pred. No. 1.6e-28;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVYKFCGCDGGLRCWESGDDPWVEHAKWPFRC 48
Db 1 PEOLASAGFYVGRNDVYKFCGCDGGLRCWESGDDPWVQHAKWPFRC 48

RESULT 13

PCT-US96-12860-10

Sequence 10, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-10

Query Match 95.6%; Score 282; DB 5; Length 48;
Best Local Similarity 93.8%; Pred. No. 1.6e-28;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVYKFCGCDGGLRCWESGDDPWVEHAKWPFRC 48
Db 1 PEOLASAGFYVGRNDVYKFCGCDGGLRCWESGDDPWVQHAKWPFRC 48

RESULT 14

US-08-511-485-26
Sequence 26, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-26

Query Match	95.6%	Score 282;	DB 2;	Length 68;
Best Local Similarity	93.8%	Pred. No. 2.3e-28;		
Matches 45; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;

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QY      1 PEOGLASAGFYVVGRRNDVKKCFCCDGGGLRCWESGDDPWYEHAKWFP RCE 48
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DB      19 PEOGLASAGFYVVGNSDDVKCFCCDGGGLRCWESGDDPWYGHAKWFP RCE 66

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RESULT 15
 US-08-511-485-6
 Sequence 6, Application US/08511485
 Patent No. 5919912
 GENERAL INFORMATION:
 APPLICANT: Korneluk, Robert G.
 APPLICANT: Mackenzie, Alexander E.
 APPLICANT: Baird, Stephen
 TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
 TITLE OF INVENTION: PROBES, AND DETECTION METHODS
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/511,485

```

1 FILING DATE: 04-AUG-1995
2 CLASSIFICATION: 514
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Clark, Paul T.
5 REGISTRATION NUMBER: 30,162
6 REFERENCE/DOCKET NUMBER: 07540/00200D
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 617/542-5070
9 TELEFAX: 617/542-8906
10 TELEX: 200154
11 INFORMATION FOR SEQ ID NO: 6:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 604 amino acids
14 TYPE: amino acid
15 STRANDEDNESS: not relevant
16 TOPOLOGY: both
17 MOLECULE TYPE: protein
18
19 US-08-511-485-6

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Query Match	95.68;	Score 282;	DB 2;	Length 604;
Best Local Similarity	93.88;	Pred. No. 2.4e-27;		
Matches 45; Conservative		2; Mismatches 1;	Indels 0;	Gaps 0;

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          ||||| : ||||| ||||| ||||| : |||||
Db      273 PEQLASAGFYVYGNSDVYKCFCCDGLRCMESGDDPMVQHAKWPFPRCE 320
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Job time : 4.26267 secs
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:50:57 ; Search time 9.45622 Seconds

(without alignments)
676.383 Million cell updates/sec

Title: US-08-569-749-9

Perfect score: 295
Sequence: 1 PEOIASAGFYVGRNDVVKC.....CWIISGDDPWVEHAKWPRCE 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	295	100.0	48	18	AAW13551	Human c-IAP1 repeat
2	295	100.0	438	17	AAW04583	Human inhibitor of
3	295	100.0	618	18	AAW19746	Human inhibitor of
4	295	100.0	618	18	AAW13545	Human c-IAP1. Hom
5	295	100.0	618	20	AAV33998	Human cellular inh
6	283	95.9	618	18	AAW19583	Human apoptosis in
7	283	95.9	618	19	AAW69296	Human HIAP-2 prote
8	283	95.9	618	23	ABG65665	Human inhibitor of
9	282	95.6	48	18	AAW13552	Human c-IAP2 repea
10	282	95.6	604	18	AAW19747	Human inhibitor of

11	282	95.6	604	18	AAW19582	Human apoptosis in
12	282	95.6	604	18	AAW13546	Human c-IAP2. Hom
13	282	95.6	604	19	AAW69295	Human HIAP-1 prote
14	282	95.6	604	20	AAV52703	Human cellular inh
15	282	95.6	604	20	AAV33997	Human cellular inh
16	282	95.6	604	23	ABG65664	Human inhibitor of
17	282	95.6	612	18	AAW13555	Murine c-IAP. Mus
18	282	95.6	612	19	AAW69299	Murine HIAP-2 prot
19	282	95.6	1140	23	AAU97837	Human cysteine pro
20	282	95.6	1141	22	AAW50694	Human API2-MLR chl
21	276	93.6	591	18	AAW19586	Mouse apoptosis in
22	276	93.6	591	23	ABG65668	Mouse inhibitor of
23	268	90.8	600	19	AAW69298	Murine HIAP-1 prot
24	262	88.8	600	23	ABG65667	Mouse inhibitor of
25	258	87.5	602	18	AAW19585	Mouse apoptosis in
26	195	66.1	68	23	AAO14943	Survivin-like prot
27	195	66.1	204	22	ABG27363	Novel human diagno
28	195	66.1	210	22	AAW25287	Human protein sequ
29	195	66.1	224	23	AAO14946	Survivin-like prot
30	195	66.1	241	23	AAO14945	Survivin-like prot
31	195	66.1	280	22	AAW31478	Amino acid sequenc
32	195	66.1	280	23	AAO14947	Survivin-like prot
33	195	66.1	298	21	AAV84907	A human proliferat
34	195	66.1	298	21	AAV69182	Human inhibitor of
35	195	66.1	355	22	AAE09457	Human SBH80014.IAP
36	188	63.7	377	22	AAE07881	Fall armyworm inh
37	185	62.7	255	22	AAE09458	Human SBH80014.IAP
38	184	62.4	263	23	ABW09488	AMPEV baculovirus
39	178	60.3	1232	17	AAV14080	Neuronal apoptosis
40	178	60.3	1295	20	AAV14080	Gonadotropic hormo
41	178	60.3	1295	20	AAV09540	Human apoptosis in
42	178	60.3	1403	18	AAW20032	Neuronal apoptosis
43	178	60.3	1403	18	AAW20033	Neuronal apoptosis
44	178	60.3	1403	20	AAV14079	Gonadotropic hormo
45	178	60.3	1403	20	AAV09539	Human apoptosis in

ALIGNMENTS

RESULT 1	AAW13551	standard; Protein: 48 AA.
ID	AAW13551	
AC	AAW13551	
XX		
DT	22-JUL-1997	(first entry)
XX		
DE	Human c-IAP1 repeat 3.	
XX		
KW	IAP: inhibitor; apoptosis; RING finger domain; restinosis;	
KW	myocardial infarction; nephritis; HIV.	
XX		
OS	Homo sapiens.	
XX		
PN	W09706182-A1.	
XX		
PD	20-FEB-1997.	
XX		
PF	06-AUG-1996;	96WO-US12860.
XX		
PR	08-DEC-1995;	95US-0569749.
XX		
PR	08-AUG-1995;	95US-0512946.
XX		
PA	(TULA-) TULARIK INC.	
XX		
PI	Goeddel DV, Rothe M;	
XX		
DR	WPI; 1997-154209/14.	
XX		
PT	Nucleic acids encoding cellular inhibitor of apoptosis proteins	
PT	useful for apoptosis regulation in cells to reduce or increase	
PT	apoptosis and for pharmacological screening	

XX Claim 3; Page 25; 35pp; English.
XX
XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
CC AAT61590/T61591) comprise a series of defined structural domain
CC repeats and/or a RING finger domain; in particular, at least two of
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
CC sequences derived from these human genes.
CC The nucleic acid is used for recombinant prodn. of human cellular
CC inhibitor of apoptosis protein which modulates apoptosis
CC regulation. The nucleic acids are useful in therapies where
CC increased cell-specific apoptosis is desired, e.g. in restenosis,
CC inflammatory disease states, myocardial infarction, glomerular
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC They can also be used in conditions requiring a reduction in
CC apoptosis.
XX
SQ Sequence 48 AA;
Query Match 100.0%; Score 295; DB 18; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.9e-29;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PEOLASAGFYVGRNDVKFCDCGGLRCWESGDDPWVHAKEPRCE 48
DB 1 PEOLASAGFYVGRNDVKFCDCGGLRCWESGDDPWVHAKEPRCE 48
RESULT 2
AAW04583
ID AAW04583 standard; Protein; 438 AA.
XX
AC AAW04583;
XX
DT 07-FEB-1997 (first entry)
XX
DE Human inhibitor of apoptosis gene 1.
XX
KW Inhibitor of apoptosis 1; hIAP-1; degenerative disease;
KW rheumatoid arthritis; septic shock; antiviral; trauma; stroke;
KW cell death; oncogenesis; cancer; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO9635703-A1.
XX
PD 14-NOV-1996.
XX
PF 11-MAY-1995; 95WO-US05922.
XX
PR 11-MAY-1995; 95WO-US05922.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI He WW, Hudson PL, Rosen CA;
XX
DR WPI; 1996-518608/51.
XX
DR N-PSDB; AAT43709.
XX
PT Polynucleotide encoding human inhibitor of apoptosis gene 1 - useful
PT for treating degenerative diseases, as antiviral defence mechanism
PT and preventing cell death during trauma and strokes
XX
PS Claim 1; Page 40-41; 53pp; English.
XX
CC Human inhibitor of apoptosis 1 (hIAP-1) (AAW04583) is a protein
CC useful for treating degenerative diseases, rheumatoid arthritis,
CC septic shock, as an antiviral defence mechanism, and for
CC preventing cell death during strokes or trauma. Its amino acid
CC sequence was deduced from a cDNA clone (AAT43709) that can be obtd.
CC from human Jurkat cell lines or human osteoclastoma stromal cell

CC lines. Recombinant hIAP-1 can be produced in prokaryotic or
CC eukaryotic host cells, or expressed in vivo. It can also be used
CC to screen for modulators of hIAP-1 activity.
XX
SQ Sequence 438 AA;
Query Match 100.0%; Score 295; DB 17; Length 438;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PEOLASAGFYVGRNDVKFCDCGGLRCWESGDDPWVHAKEPRCE 48
DB 107 PEOLASAGFYVGRNDVKFCDCGGLRCWESGDDPWVHAKEPRCE 154
RESULT 3
AAW19746
ID AAW19746 standard; Protein; 618 AA.
XX
AC AAW19746;
XX
DT 16-SEP-1997 (first entry)
XX
DE Human inhibitor of apoptosis protein homologue MIHb.
XX
KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHb;
KW degenerative disease; infectious disease; autoimmune disease;
KW cancer; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Region 46..113
FT /label= BIR
FT Region 184..250
FT /label= BIR
FT Region 269..337
FT /label= BIR
FT Region 569..606
FT /label= RING_finger
XX
PN WO9723501-A1.
XX
PD 03-JUL-1997.
XX
PF 20-DEC-1996; 96WO-AU00827.
XX
PR 22-DEC-1995; 95AU-0007275.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Vaux DL;
XX
DR WPI; 1997-350966/32.
XX
DR N-PSDB; AAT72711.
XX
PT Isolated protein homologues of viral inhibitors of apoptosis - used
PT to modulate apoptosis for treatment of degenerative, infectious or
PT autoimmune diseases and cancer
XX
PS Claim 8; Page 51-54; 136pp; English.
XX
CC Mammalian IAP homologue B (MIHb) (AAW19746) is a human homologue of
CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
CC sequence was deduced from a cDNA clone (see also AAT72711) isolated
CC from a human foetal liver cDNA library using primers based on
CC human EST sequences that resembled the BIR repeats of Oryzia
CC pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also
CC AAW19745 and AAW19747-52) and their derivatives and chemical analogues
CC can be used in methods for modulating apoptosis in animal cells,
CC specifically for treatment, by inhibition, of degenerative and
CC infectious disease or, by promotion, of cancer and autoimmune
CC disease.


```

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 46..113
FT Domain /label= BIR-1
FT Domain 184..250
FT Domain /label= BIR-2
FT Domain 269..336
FT Domain /label= BIR-3
FT Domain 560..605
FT Domain /label= Ring_zinc_finger
XX
PN WO9706255-A2.
XX
PD 20-FEB-1997.
XX
PF 05-AUG-1996; 96WO-IB01022.
XX
PR 22-DEC-1995; 95US-0576956.
PR 04-AUG-1995; 95US-0511485.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX
DR WPI; 1997-154262/14.
DR N-PSDB; AAT70838.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT of susceptibility to apoptotic disease
XX
PS Claim 27; Page 75-77; 219pp; English.
XX
XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterised by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The HIAP amino acid sequences were deduced from cDNA clones (AAT70837
CC and AAT70838) from a human liver library. IAP polypeptides can be
CC expressed in host cells (in vitro or in vivo) and used in methods
CC for treating diseases and disorders involving apoptosis, esp. in a
CC human diagnosed as HIV-positive or as having AIDS, a
CC neurodegenerative disease, a myelodysplastic syndrome or an
CC ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease.
XX
SQ Sequence 618 AA;

Query Match 95.9%; Score 283; DB 18; Length 618;
Best Local Similarity 97.9%; Pred. No. 2.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKFCDCGGLRCWESGDDPWVEHAKWPPRCE 48
    |||||||||||||||||||||||||||||||||||||||||||
DB 287 PEOLASAGFYVGRNDVKFCGCGDGLRCWESGDDPWVEHAKWPPRCE 334

RESULT 7
ID AAW69296 standard; Protein; 618 AA.
XX
AC AAW69296;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human HIAP-2 protein.
XX
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein.
XX
OS Homo sapiens.

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XX
PN WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB00781.
XX
PR 13-FEB-1997; 97US-0800929.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
PI Tsang B;
XX
DR WPI; 1998-467164/40.
DR N-PSDB; AAV55040.
XX
PT Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations
XX
PS Disclosure; Fig 3; 147pp; English.
XX
XX This sequence is the human HIAP-2 protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.
XX
SQ Sequence 618 AA;

Query Match 95.9%; Score 283; DB 19; Length 618;
Best Local Similarity 97.9%; Pred. No. 2.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKFCDCGGLRCWESGDDPWVEHAKWPPRCE 48
    |||||||||||||||||||||||||||||||||||||||||||
DB 287 PEOLASAGFYVGRNDVKFCGCGDGLRCWESGDDPWVEHAKWPPRCE 334

RESULT 8
ID ABG65665 standard; Protein; 618 AA.
XX
AC ABG65665;
XX
DT 26-AUG-2002 (first entry)
XX
DE Human inhibitor of apoptosis, HIAP2.
XX
KW Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX
OS Homo sapiens.
XX
PN WO200226968-A2.
XX
PD 04-APR-2002.

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```
XX 27-SEP-2001; 2001MO-CA01379.
PF
XX
XX 28-SEP-2000; 2000US-0672717.
PR
XX
XX (UNOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
PI
XX
XX WPI: 2002-479562/51.
DR N-PSDB; ABK93871.
DR
XX
XX Novel antisense inhibitor of apoptosis nucleic acid useful for
PT enhancing apoptosis in a cell, for treating cancer and other
PT proliferative diseases
XX
XX
XX Disclosure; Fig 3; 135pp; English.
PS
XX
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC protein sequence.
CC
XX
SQ Sequence 618 AA;
XX
XX Query Match 95.9%; Score 283; DB 23; Length 618;
XX Best Local Similarity 97.9%; Pred. No. 2.9e-26;
XX Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1 PEOLASAGFYVGRNDVKFCFCDDGLRCWESGDDPWVEHAKWPRCE 48
Db 287 PEOLASAGFYVGRNDVKFCFCDDGLRCWESGDDPWVEHAKWPRCE 334
XX
XX
XX RESULT 9
XX AAW13552
XX ID AAW13552 standard; Protein; 48 AA.
XX
XX AAW13552;
XX
XX 22-JUL-1997 (first entry)
DT
XX
XX Human c-IAP2 repeat 3.
DE
XX
XX IAP; inhibitor; apoptosis; RING finger domain; restinosis;
KW myocardial infarction; nephritis; HIV.
XX
XX Homo sapiens.
OS
XX
XX WO9706182-A1.
PN
XX
XX 20-FEB-1997.
PD
XX
XX 06-AUG-1996; 96WO-0512860.
PF
XX
XX 08-DEC-1995; 95US-0569749.
PR
XX
XX 08-AUG-1995; 95US-0512946.
XX
```

```
PA (TULA-) TULARIK INC.
XX
XX Goedel DV, Rothe M;
PI
XX
XX WPI: 1997-154209/14.
DR
XX
XX Nucleic acids encoding cellular inhibitor of apoptosis proteins
PT useful for apoptosis regulation in cells to reduce or increase
PT apoptosis and for pharmacological screening
XX
XX
XX Claim 3; Page 25; 35pp; English.
PS
XX
XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
CC AAW1590/761591) comprise a series of defined structural domain
CC repeats and/or a RING finger domain; in particular, at least two of
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
CC sequences derived from these human genes.
CC The nucleic acid is used for recombinant prodn. of human cellular
CC inhibitor of apoptosis protein which modulates apoptosis
CC regulation. The nucleic acids are useful in therapies where
CC increased cell-specific apoptosis is desired, e.g. in restinosis,
CC inflammatory disease states, myocardial infarction, glomerular
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC They can also be used in conditions requiring a reduction in
CC apoptosis.
CC
XX
XX
SQ Sequence 48 AA;
XX
XX Query Match 95.6%; Score 282; DB 18; Length 48;
XX Best Local Similarity 93.8%; Pred. No. 2.7e-27;
XX Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1 PEOLASAGFYVGRNDVKFCFCDDGLRCWESGDDPWVEHAKWPRCE 48
Db 1 PEOLASAGFYVGRNDVKFCFCDDGLRCWESGDDPWVEHAKWPRCE 48
XX
XX
XX RESULT 10
XX AAW19747
XX ID AAW19747 standard; Protein; 604 AA.
XX
XX AAW19747;
XX
XX 16-SEP-1997 (first entry)
DT
XX
XX Human inhibitor of apoptosis protein homologue MHC.
DE
XX
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MHC;
KW degenerative disease; infectious disease; autoimmune disease;
KW cancer; therapy; diagnosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 29..97
FT Region /label= BIR
FT Region 169..236
FT Region /label= BIR
FT Region 255..323
FT Region /label= BIR
FT Region 556..593
FT Region /label= RING_finger
XX
XX WO9723501-A1.
PN
XX
XX 03-JUL-1997.
PD
XX
XX 20-DEC-1996; 96WO-AU00827.
PF
XX
XX 22-DEC-1995; 95AU-0007275.
XX
```


XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
CC AAI61590/T61591) comprise a series of defined structural domain
CC repeats and/or a RING finger domain; in particular, at least two of
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
CC sequences derived from these human genes.
CC The nucleic acid is used for recombinant prodn. of human cellular
CC inhibitor of apoptosis protein which modulates apoptosis
CC regulation. The nucleic acids are useful in therapies where
CC increased cell-specific apoptosis is desired, e.g. in restinosis,
CC inflammatory disease states, myocardial infarction, glomerular
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC They can also be used in conditions requiring a reduction in
CC apoptosis.
CC
XX
SQ Sequence 604 AA:

Query Match 95.6%; Score 282; DB 16; Length 604;
Best Local Similarity 93.8%; Pred. No. 3.7e-26;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEQLASAGFYVGRNDVYKFCFCCDGLRCWESGDDPWEHAKWPRCE 48
DB 273 PEQLASAGFYVGRNDVYKFCFCCDGLRCWESGDDPWEHAKWPRCE 320

RESULT 13
AAW69295.

ID AAW69295 standard; Protein; 604 AA.

AC AAW69295;

DT 13-NOV-1998 (first entry)

DE Human HIAP-1 protein.

KM Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KM proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein.

OS Homo sapiens.

PN W09835693-A2.

PD 20-AUG-1998.

PF 13-FEB-1998; 98WO-IB00781.

PR 13-FEB-1997; 97US-0800929.

PA (UYOT-) UNIV OTTAWA.

PI Baird S, Korneluk R, liston P, Mackenzie AE, Pratt C;

PI Tsang B;

DR WPI; 1998-467164/40.

DR N-PSDB; AAV55039.

PT Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations

PS Disclosure; Fig 2; 147pp; English.

CC This sequence is the human HIAP-1 protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,

CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.

XX
SQ Sequence 604 AA:

Query Match 95.6%; Score 282; DB 19; Length 604;
Best Local Similarity 93.8%; Pred. No. 3.7e-26;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEQLASAGFYVGRNDVYKFCFCCDGLRCWESGDDPWEHAKWPRCE 48
DB 273 PEQLASAGFYVGRNDVYKFCFCCDGLRCWESGDDPWEHAKWPRCE 320

RESULT 14
AAV52703

ID AAV52703 standard; Protein; 604 AA.

AC AAV52703;

DT 26-JAN-2000 (first entry)

DE Human cellular inhibitor of apoptosis-2 protein.

KM Identification; genetic target; gene modulation; human,
KM antisense oligonucleotide; phosphorothioate; target validation;
KM nucleotide sequence-based technology; antisense drug discovery.

OS Homo sapiens.

PN W09953101-A1.

PD 21-OCT-1999.

PF 13-APR-1999; 99WO-US08268.

PR 13-APR-1998; 98US-0081483.

PR 28-APR-1998; 98US-0067638.

PA (ISIS-) ISIS PHARM INC.

PI Cowseert LM, Baker BF, McNeil J, Freier SM, Sasamor HM, Brooks DG;

PI Ohast C, Wyatt JR, Borchers AH, Vickers TA;

DR WPI; 1999-620446/53.

DR N-PSDB; AAZ41005.

PT Identifying compounds which modulate expression of nucleic acids, used
PT to provide compounds having defined physical, chemical or bioactive
PT properties, e.g. antisense activity

PS Example 20; Page 197-202; 264pp; English.

CC A method has been developed of defining a set of compounds that modulate
CC the expression of a target nucleic acid (tNA) sequence via binding of
CC the compounds with the tNA sequence. The method comprises generating a
CC library of virtual compounds in silico according to defined criteria,
CC and evaluating in silico the binding of the virtual compounds with the
CC tNA according to defined criteria. Also described are: (1) a method of
CC defining a set of oligonucleotides (ONs) that modulate the expression of
CC a tNA sequence via binding of the ONs with the tNA sequence comprising
CC generating a library of virtual compounds in silico according to defined
CC criteria, and evaluating in silico the binding of the virtual ONs with
CC the tNA according to defined criteria; and (2) a method of defining a
CC set of compounds that modulate the expression of a tNA sequence via
CC binding of the compounds with the tNA. The methods can be used for the
CC generation and identification of synthetic compounds having defined

CC physical, chemical or bioactive properties. Information gathered from
CC assays of such compounds is used to identify nucleic acid sequences that
CC are tractable to a variety of nucleotide sequence-based technologies,
CC e.g. antisense drug discovery and target validation. AA240852 to
CC AA241220, and AA52701 to AA52706, represent sequences used in the
CC exemplification of the present invention.

XX Sequence 604 AA;

Query Match

Best Local Similarity 95.6%; Score 282; DB 20; Length 604;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVYHAKWPRCE 48
||||| :|||||
DB 273 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVYHAKWPRCE 320

RESULT 15

AY33997
ID AAY33997 standard; Protein; 604 AA.

AC AAY33997;

DT 26-NOV-1999 (first entry)

DE Human cellular inhibitor of apoptosis-2 sequence.

KW Cellular inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;
c-IAP-2; prophylaxis; infection; inflammation; tumor formation.

OS Homo sapiens.

PN US5958771-A.

PD 28-SEP-1999.

PF 03-DEC-1998; 98US-0205144.

PR 03-DEC-1998; 98US-0205144.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowser LM, Ackermann EJ;

DR WPI; 1999-561046/47.

DR N-PSDB; AA22096.

PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2
XX useful for e.g. diagnostics, therapeutics, and as research reagents -
XX Example 13: Columns 45-50; 33pp; English.

CC The invention provides antisense compounds of 8-30 nucleotides that
CC inhibit the expression of human Cellular Inhibitor of Apoptosis-2
CC (c-IAP-2). The antisense compounds may be used for diagnostics,
CC therapeutics (for modulating the expression of c-IAP-2), prophylaxis
CC (e.g. to prevent or delay infection, inflammation, or tumor formation),
CC as research reagents (e.g. to distinguish between members of a biological
CC pathway) and in kits. The present sequence represents the human cellular
CC inhibitor of apoptosis-2.

XX Sequence 604 AA;

Query Match

Best Local Similarity 95.6%; Score 282; DB 20; Length 604;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVYHAKWPRCE 48
||||| :|||||
DB 273 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVYHAKWPRCE 320

Search completed: May 5, 2003, 16:02:02
Job time : 10.4562 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:58:42 ; Search time 5.25346 Seconds

(without alignments)
878.365 Million cell updates/sec

Title: US-08-569-749-9

Perfect score: 295

Sequence: 1 PEOLASAGFYVGRNDVYKC.....CWISGDDPWVHAKEPPRCE 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	283	95.9	618	2	S68450 apoptosis inhibitor
2	282	95.6	358	2	JC5964 apoptosis inhibitor
3	282	95.6	604	2	S68449 apoptosis inhibitor
4	198	67.1	268	2	T10304 inhibitor of apopt
5	198	67.1	268	2	A53989 apoptosis-inhibiti
6	195	66.1	298	2	JC7568 kidney inhibitor o
7	183	62.0	1447	2	T42628 neuronal apoptosis
8	182	61.7	275	2	A45679 inhibitor-of-apopt
9	178	60.3	1232	2	A55478 neuronal apoptosis
10	174	59.0	497	2	S69544 apoptosis inhibito
11	156	52.9	496	2	S68452 apoptosis inhibito
12	156	52.9	497	2	S69545 apoptosis inhibito
13	119	40.3	150	2	T28409 ORF MSV248 probabl
14	118	40.0	286	2	D36828 orf13 protein - Au
15	117.5	39.8	4845	2	T31067 BIR repeat contain
16	115	39.0	292	2	T41772 IAP1 orf27 - Bomby
17	111	37.6	275	2	T10310 apoptosis-inhibiti
18	110	37.3	208	2	T03183 probable apoptosis
19	104	35.3	997	2	T43523 cutl7 protein - fi
20	100	33.9	155	2	T30489 apoptosis inhibito
21	79	26.8	155	2	T37471 apoptosis inhibito
22	77	26.1	308	2	T37474 apoptosis inhibito
23	71	24.1	234	2	T30427 probable apoptosis
24	64.5	21.9	329	2	T28403 ORF MSV242 probabl
25	64.5	21.9	772	2	D96504 protein F9C16.25 f
26	62	21.0	287	2	T05358 hypothetical prote
27	58.5	19.8	743	2	T02147 hypothetical prote
28	58	19.7	556	2	A32466 numb protein - fru
29	57.5	19.5	156	2	A48866 8-oxo-7,8-dihydrog

30	57.5	19.5	555	2	B49918 schC protein - Str
31	56.5	19.2	485	2	E89859 D-alanine-D-alanyl
32	56	19.0	65	2	A38739 metallothionein -
33	56	19.0	281	2	T13340 probable lysin - S
34	56	19.0	436	2	E88499 protein K0467.4 f1
35	55.5	18.8	703	2	T04191 hypothetical prote
36	55.5	18.6	1536	1	RGBYS3 regulatory protein
37	55	18.6	92	2	S34802 embryonic abunda
38	55	18.6	92	2	S71372 embryonic abunda
39	55	18.6	625	2	T01929 probable cellulase
40	55	18.6	954	2	S57108 hypothetical prote
41	55	18.6	3229	2	S27852 probable cell-surf
42	54.5	18.5	249	2	H72858 apoptosis inhibito
43	54.5	18.5	249	2	T41814 IAP2 orf71 - Bomby
44	54.5	18.5	415	2	C71467 probable tyrosine
45	54.5	18.5	547	2	A36046 collagen alpha cha

ALIGNMENTS

RESULT 1
S68450
apoptosis inhibitor hlap-2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68450
R:Ristow, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahe
Nature 379, 349-353, 1996.
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <LIS>
A:Cross-references: EMBL:045879; NID:91184317; PIDN:AAC50372.1; PID:91184318
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:567-611/Domain: RING finger homology <RNG>

Query Match 95.9%; Score 283; DB 2; Length 618;
Best Local Similarity 97.9%; Pred. No. 1.7e-25;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVYKCFCDCGGLRCWESGDDPWVHAKEPPRCE 48
DB 287 PEOLASAGFYVGRNDVYKFCGCDGGLRCWESGDDPWVHAKEPPRCE 334

RESULT 2
JC5964
apoptosis inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Sep-2000
C:Accession: JC5964
R:Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap)
A:Reference number: JC5964; MUID:98162622; PMID:9501011
A:Accession: JC5964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>
A:Cross-references: GB:079142; NID:92957174; PIDN:AAC39171.1; PID:92957175
C:Superfamily: RING finger homology
F:307-351/Domain: RING finger homology <RRN>

Query Match 95.6%; Score 282; DB 2; Length 358;
Best Local Similarity 93.8%; Pred. No. 1.3e-25;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 12
S69545

apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69545
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan, M.C.
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A:Reference number: S69544; MUID:96236286; PMID:8654366
A:Accession: S69545
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: EMBL:U032373; NID:91019116; PIDN:AAC47155.1; PID:91019117
C:Genetics:
A:Gene: i1p
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
F:446-490/Domain: RING finger homology <RRN>

Query Match 52.9%; Score 156; DB 2; Length 497;
Best Local Similarity 55.6%; Pred. No. 1e-10;
Matches 25; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 4 LASAGFYVGRNDVKCFCCDGLRCWESGDDPWVEHAKWPRCE 48
Db 233 LAQAGLYYKIGDQVRCFHCNIGLRSMQKEDERPVEHAKWPRCKQ 277

RESULT 13

ORF MSV248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes entomoc
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T28409
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359
A:Accession: T28409
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-150 <AFO>
A:Cross-references: EMBL:AF063866; NID:94049647; PIDN:AAC97724.1; PID:94049764
C:Genetics:
A:Note: MSV248

Query Match 40.3%; Score 119; DB 2; Length 150;
Best Local Similarity 42.2%; Pred. No. 7.6e-07;
Matches 19; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 3 QLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVEHAKWPRC 47
Db 36 RICEAGFFYTNIGDITVCFCGKIKKMLYNDPWIHSKWSKSPNC 80

RESULT 14

orf13 protein - Autographa californica nuclear polyhedrosis virus
C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Nov-2000
C:Accession: D36828; C72853
R:Braunagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.
Virology 191, 1003-1008, 1992
A:Title: Sequence, genomic organization of the ECOR1-A fragment of Autographa californic
VP8 of rotavirus.
A:Reference number: A44221; MUID:93079853; PMID:1333113
A:Accession: D36828
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <BRA>

A:Cross-references: GB:S52569
R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus

A:Reference number: A72850; MUID:94303173; PMID:8030224

A:Accession: C72853
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199, 'L', 201-286 <AYR>
A:Cross-references: GB:I22858; NID:9510708; PIDN:AAA6657.1; PID:9559096
C:Genetics:
A:Gene: Ac-IAP1
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 40.0%; Score 118; DB 2; Length 286;
Best Local Similarity 43.2%; Pred. No. 1.8e-06;
Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 4 LASAGFYVGRNDVKCFCCDGLRCWESGDDPWVEHAKWPRC 47
Db 153 IAEAGLYYRGDETVCFCCDCCVRRWHTNEDTWORHAENPQC 196

RESULT 15

T31067
BIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T31067
R:Hauser, H.P.; Bardoff, M.; Pyrowolakis, G.; Jentsch, S.
J. Cell Biol. 141, 1415-1422, 1998
A:Title: A giant ubiquitin-conjugating enzyme related to IAP apoptosis inhibitors.
A:Reference number: Z20963; MUID:98292517; PMID:9628897
A:Accession: T31067
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4845 <HAU>
A:Cross-references: EMBL:Y17267; NID:93319989; PIDN:CAAT6720.1; PID:93319990
A:Note: localized to the Golgi compartment and the vesicular system
C:Keywords: membrane-associated protein

Query Match 39.8%; Score 117.5; DB 2; Length 4845;
Best Local Similarity 42.0%; Pred. No. 2.7e-05;
Matches 21; Conservative 6; Mismatches 20; Indels 3; Gaps 1;

QY 1 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVEHAKWPRC 47
Db 281 PDPMAQAGFYHQPASSGDDRAMCFCTSCVLCVWEPPDEPWESEHERHSPNC 330

Search completed: May 5, 2003, 16:08:13
Job time: 7.25346 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:07 ; Search time 5.91705 Seconds

(Without alignments)
699.970 Million cell updates/sec

Title: US-08-569-749-9

Perfect score: 295
Sequence: 1 PEQLASAGFYVGRNDVKC.....CWESGDDPWVTEHAKWPRCE 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PC1_NIW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PC1US_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	295	100.0	438	1	US-08-464-588-2
2	283	95.9	68	9	US-09-201-936-27
3	283	95.9	618	9	US-09-201-936-8
4	283	95.9	618	10	US-09-974-592-8
5	282	95.6	68	9	US-09-201-936-26
6	282	95.6	604	9	US-09-201-936-6
7	282	95.6	604	10	US-09-974-592-6
8	282	95.6	612	10	US-09-974-592-14
9	276	93.6	591	9	US-09-201-936-42
10	268	90.8	600	10	US-09-974-592-12
11	262	88.8	602	9	US-09-201-936-40
12	198	67.1	68	9	US-09-201-936-28
13	198	67.1	68	9	US-10-041-859-18
14	198	67.1	172	9	US-10-041-859-12
15	192	65.1	68	9	US-10-041-859-14
16	192	65.1	172	9	US-10-041-859-8
17	192	65.1	346	9	US-10-041-859-2
18	189	64.1	68	9	US-10-041-859-16
19	189	64.1	172	9	US-10-041-859-10

20	188	63.7	68	9	US-10-041-859-15	Sequence 15, Appl
21	188	63.7	172	9	US-10-041-859-9	Sequence 9, Appl
22	182	61.7	68	9	US-09-201-936-29	Sequence 29, Appl
23	182	61.7	68	9	US-10-041-859-17	Sequence 17, Appl
24	182	61.7	172	9	US-10-041-859-11	Sequence 11, Appl
25	182	61.7	275	9	US-09-201-936-12	Sequence 12, Appl
26	178	60.3	1403	8	US-08-913-322-22	Sequence 22, Appl
27	178	60.3	1403	8	US-08-913-322-24	Sequence 24, Appl
28	174	59.0	66	9	US-09-201-936-25	Sequence 25, Appl
29	174	59.0	107	9	US-09-965-967-20	Sequence 20, Appl
30	174	59.0	278	9	US-09-964-899-39	Sequence 39, Appl
31	174	59.0	497	9	US-09-201-936-4	Sequence 4, Appl
32	174	59.0	497	10	US-09-974-592-4	Sequence 4, Appl
33	160	54.2	66	9	US-09-201-936-24	Sequence 24, Appl
34	160	54.2	68	9	US-10-041-859-19	Sequence 19, Appl
35	160	54.2	109	9	US-09-965-967-30	Sequence 30, Appl
36	160	54.2	172	9	US-10-041-859-13	Sequence 13, Appl
37	160	54.2	496	9	US-09-201-936-10	Sequence 10, Appl
38	160	54.2	496	10	US-09-974-592-10	Sequence 10, Appl
39	159	53.9	68	9	US-09-201-936-20	Sequence 20, Appl
40	156	52.9	68	9	US-09-201-936-21	Sequence 21, Appl
41	156	52.9	68	9	US-09-201-936-30	Sequence 30, Appl
42	156	52.9	110	9	US-09-965-967-21	Sequence 21, Appl
43	156	52.9	498	9	US-09-201-936-13	Sequence 13, Appl
44	144	48.8	67	9	US-09-201-936-14	Sequence 14, Appl
45	142	48.1	67	9	US-09-201-936-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-464-588-2
Sequence 2, Application US/08464588
Publication No. US20030073159A1
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,588
FILING DATE: June 5, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922
FILING DATE: 11 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-387
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN

US-08-464-588-2

Query Match 100.0%; Score 295; DB 1; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKFCFCCDGGGRCWESGDDPWVEHAKWPFRC 48
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DB 107 PEOLASAGFYVGRNDVYKFCFCCDGGGRCWESGDDPWVEHAKWPFRC 154

RESULT 2

US-09-201-936-27
; Sequence 27, Application US/09201936
; Publication No. US20020187946A1

; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/TB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-27

Query Match 95.9%; Score 283; DB 9; Length 68;
Best Local Similarity 97.9%; Pred. No. 4.8e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKFCFCCDGGGRCWESGDDPWVEHAKWPFRC 48
|||||
DB 19 PEOLASAGFYVGRNDVYKFCFCCDGGGRCWESGDDPWVEHAKWPFRC 66

RESULT 3

US-09-201-936-8
; Sequence 8, Application US/09201936
; Publication No. US20020187946A1

; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-01
; EARLIER APPLICATION NUMBER: PCT/TB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-8

Query Match 95.9%; Score 283; DB 9; Length 618;
Best Local Similarity 97.9%; Pred. No. 4.1e-25;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKFCFCCDGGGRCWESGDDPWVEHAKWPFRC 48
|||||
DB 287 PEOLASAGFYVGRNDVYKFCFCCDGGGRCWESGDDPWVEHAKWPFRC 334

RESULT 4

US-09-974-592-8
; Sequence 8, Application US/09974592
; Patent No. US20020120121A1

; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-8

Query Match 95.9%; Score 283; DB 10; Length 618;
Best Local Similarity 97.9%; Pred. No. 4.1e-25;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKFCFCCDGGGRCWESGDDPWVEHAKWPFRC 48
|||||
DB 287 PEOLASAGFYVGRNDVYKFCFCCDGGGRCWESGDDPWVEHAKWPFRC 334

RESULT 5

US-09-201-936-26
; Sequence 26, Application US/09201936
; Publication No. US20020187946A1

; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-01
; EARLIER APPLICATION NUMBER: PCT/TB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956

FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42
LENGTH: 591
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-936-42

Query Match 93.6%; Score 276; DB 9; Length 591;
Best Local Similarity 91.7%; Pred. No. 2.5e-24;
Matches 44; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 48
Db 259 PEOLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 306

RESULT 10
US-09-974-592-12
Sequence 12, Application US/09974592
Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratl, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 600
TYPE: PRT
ORGANISM: Mus musculus
US-09-974-592-12

Query Match 90.8%; Score 268; DB 10; Length 600;
Best Local Similarity 89.4%; Pred. No. 2.2e-23;
Matches 42; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 EOLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 48
Db 272 EOLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 318

RESULT 11
US-09-201-936-40
Sequence 40, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.

APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 40
LENGTH: 602
TYPE: PRT
ORGANISM: Mus musculus
US-09-201-936-40

Query Match 88.8%; Score 262; DB 9; Length 602;
Best Local Similarity 87.2%; Pred. No. 1.1e-22;
Matches 41; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 EOLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 48
Db 274 EOLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 320

RESULT 12
US-09-201-936-28
Sequence 28, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 68
TYPE: PRT
ORGANISM: Oryzias pseudotsugata
US-09-201-936-28

Query Match 67.1%; Score 198; DB 9; Length 68;
Best Local Similarity 60.4%; Pred. No. 3.6e-16;
Matches 29; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 48
Db 19 PEOLASAGFYVGRNDVCKFCDCGGLRCWESGDDPWVEHAKWPRCE 66

RESULT 13
US-10-041-859-18

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; Sequence 18, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Oryza pseudotsugata
US-10-041-859-18
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Query Match 67.1%; Score 198; DB 9; Length 68;
Best Local Similarity 60.4%; Pred. No. 3.6e-16;
Matches 29; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
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OY 1 PEOLASAGFYVGRNDVKKFCDCDGLRCWESGDDPWVEHAKWPPRC 48
DB 19 PEELAEAGFFYTGQDKTRCFCCDGLKDWESDDVPWQOHARWYDRCE 66
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RESULT 14
US-10-041-859-12
; Sequence 12, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Oryza pseudotsugata
US-10-041-859-12
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Query Match 67.1%; Score 198; DB 9; Length 172;
Best Local Similarity 60.4%; Pred. No. 8.9e-16;
Matches 29; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
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OY 1 PEOLASAGFYVGRNDVKKFCDCDGLRCWESGDDPWVEHAKWPPRC 48
DB 86 PEELAEAGFFYTGQDKTRCFCCDGLKDWESDDVPWQOHARWYDRCE 133
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RESULT 15
US-10-041-859-14
; Sequence 14, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
```

```
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Bombyx mori
US-10-041-859-14
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Query Match 65.1%; Score 192; DB 9; Length 68;
Best Local Similarity 63.8%; Pred. No. 1.8e-15;
Matches 30; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
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OY 1 PEOLASAGFYVGRNDVKKFCDCDGLRCWESGDDPWVEHAKWPPRC 47
DB 19 PEELAEAGFFYTGQDKTRCFCCDGLKDWESDDVPWQOHARWYDRCE 65
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Search completed: May 5, 2003, 16:11:07
Job time : 6.91705 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:57:12 ; Search time 11.7235 Seconds

(Without alignments)
843.627 Million cell updates/sec

Title: US-08-569-749-9

Sequence: 1 PEQLASAGFYVGRNDVKC.....CWSSGDDPWVEHAKWFPFCE 48

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacterioplasmid:*
17: sp_archaeoplasmid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290	98.3	195	13	Q9IA70
2	290	98.3	197	13	Q9IA69
3	290	98.3	610	13	057319
4	288	97.6	628	13	Q8UWD2
5	277	93.9	589	11	Q9ESE8
6	277	93.9	589	11	Q9OEC6
7	275	93.2	602	11	Q9ESE9
8	271	91.9	324	13	Q9DND2
9	268	90.8	374	11	Q921N0
10	209	70.8	224	11	Q86642
11	198	67.1	264	12	Q9EN27
12	195	66.1	280	4	Q9HAP7
13	195	66.1	298	4	Q9H2A8
14	195	66.1	298	4	Q96CA5
15	192	65.1	281	12	Q9YML8
16	192	65.1	346	5	Q968T8

17	192	65.1	405	13	Q8UWH2	Q8UWH2 brachydantio
18	189	64.1	379	5	Q9U492	Q9U492 trichoplusi
19	188	63.7	377	5	Q9NJ07	Q9NJ07 spodoptera
20	186	63.1	276	12	Q89744	Q89744 buzzara supp
21	186	63.1	313	12	Q9J827	Q9J827 spodoptera
22	186	63.1	597	11	Q9R015	Q9R015 mus musculu
23	185	62.7	276	12	Q8QJ95	Q8QJ95 mamestra co
24	178	60.3	403	5	Q8WR99	Q8WR99 ochlerotatu
25	177	60.0	402	5	Q8T621	Q8T621 aedes albop
26	174	59.0	496	11	Q9ESF0	Q9ESF0 rattus norv
27	174	59.0	501	11	Q9E005	Q9E005 rattus norv
28	174	59.0	501	11	Q9E004	Q9E004 rattus norv
29	171	58.0	236	4	Q96RW5	Q96RW5 homo sapien
30	171	58.0	236	4	Q96P09	Q96P09 homo sapien
31	171	58.0	236	6	Q95M72	Q95M72 pan troglod
32	171	58.0	261	12	Q9OES9	Q9OES9 epiphyas po
33	170	57.6	236	6	Q95M71	Q95M71 gorilla gor
34	166	56.3	493	13	Q8UVE8	Q8UVE8 gallus gall
35	161	54.6	106	4	Q96RW6	Q96RW6 homo sapien
36	160	54.2	438	5	Q9VUX5	Q9VUX5 drosophila
37	156	52.9	498	5	Q96OU3	Q96OU3 drosophila
38	138	46.8	517	11	Q8R4U8	Q8R4U8 rattus norv
39	131	44.4	268	12	Q9RFR8	Q9RFR8 helioverpa
40	131	44.4	268	12	Q9E232	Q9E232 helioverpa
41	130.5	44.2	153	5	Q9VEN2	Q9VEN2 drosophila
42	130	44.1	1160	4	Q8TDX4	Q8TDX4 homo sapien
43	121.5	41.2	4904	5	Q9VH01	Q9VH01 drosophila
44	121	41.0	243	12	Q91EW1	Q91EW1 cydia pomon
45	119	40.3	150	12	Q9YVJ4	Q9YVJ4 melanoplus

ALIGNMENTS

RESULT 1	Q9IA70	PRELIMINARY;	PRT;	195 AA.
ID	Q9IA70			
AC	Q9IA70;			
DT	01-OCT-2000 (TREMREL. 15, Created)			
DT	01-OCT-2000 (TREMREL. 15, Last annotation update)			
DT	01-DEC-2001 (TREMREL. 19, Last annotation update)			
DE	Inhibitor of apoptosis 1 (Fragment).			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRED LEHORN; TISSUE=SPLEEN;			
RX	MEDLINE-21158006; PubMed-11261557;			
RA	Zhou H., Liu W., Lamont S.J.;			
RT	"Genetic variation among chicken lines and mammalian species in			
RT	specific genes";			
RL	Poult. Sci. 80:284-288(2001).			
DR	EMBL; AF221082; AAF35319.1; -.			
DR	HSSP: Q13490; IOBH.			
DR	InterPro: IPR001370; BIR.			
DR	Pfam: PF00653; BIR; 2.			
DR	SMART; SM00238; BIR; 2.			
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.			
DR	PROSITE; PS0143; BIR_REPEAT_2; 2.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	195 AA;	22347 MW;	9C39BFA755E24E48 CRC64;
Query Match		98.3%;	Score 290;	DB 13; Length 195;
Best Local Similarity		95.8%;	Pred. No. 1e-30;	
Matches	46;	Conservative	1;	Mismatches 1; Indels 0; Gaps 0;
QY	1	PEQLASAGFYVGRNDVKCFCCDGGGLRCWESGDDPWVEHAKWFPFCE 48		
DB	134	PEQLADAGFYVGRNDVKCFCCDGGGLRCWESGDDPWVEHAKWFPFCE 181		

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RESULT 2
O91A69 ID O91A69 PRELIMINARY; PRT; 197 AA.
AC O91A69;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRED FAYOUMI; TISSUE=SPLEEN;
RX MEDLINE=21158006; Pubmed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
RT specific genes."
RL Poul. Sci. 80:284-288(2001).
DR EMBL; AF221083; AAF35320.1; -.
DR HSSP; O13490; IOBH.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1 1
FT 197 197
SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match 98.3%; Score 290; DB 13; Length 197;
Best Local Similarity 95.8%; Pred. No. 1e-30;
Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOIASAGFYVGRNDVKFCGCCDGLRCWESGDDPWVIEHAKWPRCE 48
DB 135 PEOIADAGFYVGRNDVKFCGCCDGLRCWESGDDPWVIEHAKWPRCE 182

RESULT 3
O57319 ID O57319 PRELIMINARY; PRT; 610 AA.
AC O57319;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Inhibitor of apoptosis protein 1 (IAP) (Inhibitor of T cell apoptosis
DE PROTEIN).
GN IAP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LECHORN; TISSUE=EMBRYONIC FIBROBLAST;
RX MEDLINE=98038801; Pubmed=9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
RT mediator of the antiapoptotic activity of the v-rel oncoprotein."
RL Mol. Cell. Biol. 17:7328-7341(1997).
CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CC CELLS.
CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
CC THE V-REL-TRANSFORMED CELLS.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
CC SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
CC IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
```

```
CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC PROCESS.
CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
CC APOPTOSIS PROTEIN REPEAT).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; AF008592; AAB88044.1; -.
DR HSSP; O13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
KM Apoptosis; Zinc-finger; Repeat.
FT REPEAT 30 97 BIR REPEAT 1.
FT REPEAT 176 242 BIR REPEAT 2.
FT REPEAT 262 329 BIR REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADF47619650B44A6 CRC64;

Query Match 98.3%; Score 290; DB 13; Length 610;
Best Local Similarity 95.8%; Pred. No. 3.4e-30;
Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOIASAGFYVGRNDVKFCGCCDGLRCWESGDDPWVIEHAKWPRCE 48
DB 280 PEOIADAGFYVGRNDVKFCGCCDGLRCWESGDDPWVIEHAKWPRCE 327

RESULT 4
Q8UWD2 ID Q8UWD2 PRELIMINARY; PRT; 628 AA.
AC Q8UWD2;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Iap1.
GN IAP1.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20373792; Pubmed=10917738;
RX Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC Inohara N., Nunez G.;
RX Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF442500; AAL33679.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
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Db 273 PQELASAGFYTGSHSDVKCFCCDGLRCWESGDDPWVEHAKWEP RCE 320

RESULT 8

Q9DDN2 PRELIMINARY; PRT; 324 AA.
AC Q9DDN2;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Apoptosis inhibitor ch-IAP1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;
RT "The apoptosis inhibitor ch-IAP1 is a direct transcriptional target of
v-Rel and c-Rel."
RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF311289; AAC42316.1; -
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
FT NON_TER 324
SQ SEQUENCE 324 AA; 36567 MW; 5E2B89DEAE3733F3 CRC64;

Query Match 91.9%; Score 271; DB 13; Length 324;
Best Local Similarity 95.6%; Pred. No. 5.8e-28;
Matches 43; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PQELASAGFYTGSHSDVKCFCCDGLRCWESGDDPWVEHAKWEP 45
Db 280 PQELASAGFYTGSHSDVKCFCCDGLRCWESGDDPWVEHAKWEP 324

RESULT 9

Q921N0 PRELIMINARY; PRT; 374 AA.
AC Q921N0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Similar to baculoviral IAP repeat-containing 2.
GN BIRC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011338; AAH1338.1; -
DR MGI: 1197007; Birc2.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 90.8%; Score 268; DB 11; Length 374;
Best Local Similarity 89.4%; Pred. No. 1.7e-27;
Matches 42; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQELASAGFYTGSHSDVKCFCCDGLRCWESGDDPWVEHAKWEP RCE 48
Db 272 PQELASAGFYTGSHSDVKCFCCDGLRCWESGDDPWVEHAKWEP RCE 318

RESULT 10

O88642 PRELIMINARY; PRT; 224 AA.
AC O88642;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein (Fragment).
GN RIAP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-WISTAR; TISSUE-OVARY;
RA Bradley C.K., Lareu R.R., Dharmarajan A.M.;
RT "Cloning and characterisation of an inhibitor of apoptosis protein
(IAP) in the rat corpus luteum."
RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF081503; AAC32497.1; -
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 224 AA; 25209 MW; 213A52534D5EB56A CRC64;

Query Match 70.8%; Score 209; DB 11; Length 224;
Best Local Similarity 91.9%; Pred. No. 6.8e-20;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PQELASAGFYTGSHSDVKCFCCDGLRCWESGDDPW 37
Db 188 PQELASAGFYTGSHSDVKCFCCDGLRCWESGDDPW 224

RESULT 11

Q9EN27 PRELIMINARY; PRT; 264 AA.
AC Q9EN27;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE AMV021.
GN AMV021.
OS Amsacta moorei entomopoxvirus (AmePV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
OX NCBI_TaxID=28321;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20396580; PubMed=10936094;
RA Bawden A.L., Glassberg K.J., Digans J., Shaw R., Farmerie W.,
Moyer R.W.;
RT "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
Analysis and Comparison with Other Poxviruses."
RT Virology 274:120-139(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Bawden A.L., Glassberg K.J., Digans J., Shaw R., Farmerie W.,
Moyer R.W.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF250284; AAG02727.1; -
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.

DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
SQ SEQUENCE 264 AA; 30547 MW; 2EB72DA4B58D920A CRC64;

Query Match 67.1%; Score 198; DB 13; Length 264;
Best Local Similarity 61.7%; Pred. No. 2.4e-18;
Matches 29; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 2 EOLASAGFYVGRNDVYKFCDCGGLRCWESGDDPWVHAHAKWPRCE 48
DB 126 EKLAEAGFYTGKSDVKKCFYCDGLNKMTETDDDPWIOAHAKWPRCKD 172

RESULT 12

Q9HAP7 PRELIMINARY; PRT; 280 AA.
AC Q9HAP7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Livin inhibitor of apoptosis (inhibitor of apoptosis) (BA261N1.1.1)
DE (Baculoviral IAP repeat-containing protein 7 (Livin), isoform 1).
GN LIVIN OR BIRC7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kasof G.M., Gomes B.C.;
RT "Livin, a novel inhibitor of apoptosis (IAP) family member.";
RL J. Biol. Chem. 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Ashhab Y., Allan A., Pollack A., Panet A., Ben-Yehuda D.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
RT different biological properties and tissue distribution pattern.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hall R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF31388; AAG33622.1; -;
DR EMBL; AJ309298; CAC37337.1; -;
DR EMBL; AL121827; CAC36112.1; -;
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_rling.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
KW Zinc-finger.
SQ SEQUENCE 280 AA; 30865 MW; 630BE9C0737F7952 CRC64;

Query Match 66.1%; Score 195; DB 4; Length 280;
Best Local Similarity 62.5%; Pred. No. 6.3e-18;
Matches 30; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKFCDCGGLRCWESGDDPWVHAHAKWPRCE 48
DB 105 PELLAAGFFHTGHQDKVRCFCYGLQSWKRGDDPWTEHAKWPRSCQ 152

RESULT 13
Q9H2A8 PRELIMINARY; PRT; 298 AA.
AC Q9H2A8;

DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein KIAA (BA261N1.1.2) (Baculoviral IAP
DE repeat-containing protein 7 (Livin), isoform 2).
GN BIRC7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin J.-H., Deng G., Huang Q., Morser J.;
RT "A Novel member of the inhibitor of apoptosis protein family.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Ashhab Y., Allan A., Pollack A., Panet A., Ben-Yehuda D.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
RT different biological properties and tissue distribution pattern.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hall R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF301009; AAG37878.1; -;
DR EMBL; AJ309298; CAC37338.1; -;
DR EMBL; AL121827; CAC36111.1; -;
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_rling.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
KW Zinc-finger.
SQ SEQUENCE 298 AA; 32798 MW; B2EAAE531BEC101 CRC64;

Query Match 66.1%; Score 195; DB 4; Length 298;
Best Local Similarity 62.5%; Pred. No. 6.7e-18;
Matches 30; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVYKFCDCGGLRCWESGDDPWVHAHAKWPRCE 48
DB 105 PELLAAGFFHTGHQDKVRCFCYGLQSWKRGDDPWTEHAKWPRSCQ 152

RESULT 14

Q96CA5 PRELIMINARY; PRT; 298 AA.
AC Q96CA5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to baculoviral IAP repeat-containing 7 (Livin).
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Skin;
RC Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC014475; AAH14475.1; -;
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_rling.

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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 1.99078 Seconds

(without alignments)
1000.040 Million cell updates/sec

Title: US-08-569-749-9

Perfect score: 295

Sequence: 1 PEQLASGFFYYVGRNDVKC.....CWESGDDPWVHAKFPFCE 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295	100.0	618	BIR3_HUMAN	Q13490 homo sapien
2	290	98.3	611	BIR_CHICK	Q90660 gallus gall
3	282	95.6	358	PIAP_PIG	Q62640 sus scrofa
4	282	95.6	604	BIR2_HUMAN	Q13489 homo sapien
5	282	95.6	612	BIR3_MOUSE	Q62210 mus musculu
6	268	90.8	600	BIR2_MOUSE	Q08863 mus musculu
7	198	67.1	268	IAP3_NPVOP	P41437 orgyia pseu
8	195	66.1	298	BIR7_HUMAN	Q96ca5 homo sapien
9	187	63.4	1403	BIRF_MOUSE	Q9j1b6 mus musculu
10	186	63.1	1402	BIRG_MOUSE	Q9j1b3 mus musculu
11	186	63.1	1403	BIRA_MOUSE	Q9qwk5 mus musculu
12	186	63.1	1403	BIRE_MOUSE	Q9qwk5 mus musculu
13	183	62.0	1447	BIRB_MOUSE	Q9j016 mus musculu
14	182	61.7	275	IAP_GVCP	P41436 cydia pomon
15	178	60.3	1403	BIR1_HUMAN	Q13075 homo sapien
16	174	59.0	496	BIR4_MOUSE	Q60989 mus musculu
17	174	59.0	496	BIR4_RAT	Q9j016 rattus norv
18	174	59.0	497	BIR4_HUMAN	P98170 homo sapien
19	171	58.0	236	BIR8_HUMAN	Q96P09 homo sapien
20	171	58.0	236	BIR8_PANTR	Q95m72 pan troglod
21	170	57.6	236	BIR8_GORGO	Q95m71 gorilla gor
22	160	54.2	438	IAP1_DROME	Q24307 drosophila
23	156	52.9	498	IAP2_DROME	Q24306 drosophila
24	118	40.0	286	IAP1_NPVAC	P41435 autographa
25	117.5	39.8	4829	BIR6_HUMAN	Q9hr09 homo sapien
26	111	37.6	275	IAP1_NPVOP	O10296 orgyia pseu
27	110	37.3	239	ZFP_TRV6	P47732 chilo tride
28	104	35.3	997	BIR1_SCHFO	O14064 schizosacch
29	90.5	30.7	140	BIR5_MOUSE	Q07201 mus musculu
30	90.5	30.7	142	BIR5_RAT	Q9jhy7 rattus norv
31	87.5	29.7	142	BIR5_HUMAN	O13392 homo sapien
32	67.5	22.9	224	IAP1_ASFB7	O65138 african swi
33	65.5	22.2	224	IAP1_ASFMI	O11452 african swi

34	61.5	20.8	224	1	IAP1_ASFC3	O11451 african swi
35	61.5	20.8	224	1	IAP1_ASFC3	O12407 african swi
36	61.5	20.8	238	1	IAP1_ASFM2	O11453 african swi
37	58.5	19.8	1173	1	TSPL_XENLA	P35448 xenopus lae
38	58	19.7	68	1	MT_LTYPI	O02033 lytechinus
39	58	19.7	556	1	NUMB_DROME	P16554 drosophila
40	57.5	19.5	156	1	8ODP_HUMAN	P36639 homo sapien
41	57.5	19.5	555	1	HYDL_STRHA	Q05355 streptomyc
42	57	19.3	1004	1	PO1L_SCICO	Q03277 sclara copr
43	56	19.0	65	1	MTB_STRPU	Q27287 strongyloce
44	55.5	18.8	1202	1	JAG2_RAT	P97607 rattus norv
45	55.5	18.8	1247	1	JAG2_MOUSE	Q9qye5 mus musculu

ALIGNMENTS

RESULT 1
BIR3_HUMAN STANDARD; PRT: 618 AA.
AC Q13490; Q16516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis protein 2) (IAP homolog B).
DE protein 2) (IAP homolog B).
GN BIRC3 OR API2 OR IAP2 OR MIH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP MEDLINE:96128127; PubMed:8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
RG Cell 83:1243-1252(1995);
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE:96149249; PubMed:8552191;
RA Liston P., Roy N., Tamai K., Lefevre C., Baird S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE:96209843; PubMed:8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls R.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RA Strausberg R.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP STRUCTURE BY NMR OF 266-363.
RX MEDLINE:9932054; PubMed:10404221;
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat.";
RL Nat. Struct. Biol. 6:648-651(1999).
CC -I- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

```
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC Inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chiromancer/Genes/BIRC3ID239.html".
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DR EMBL: L49431; AAC41942.1; -
DR EMBL: U45879; AAC50372.1; -
DR EMBL: U37547; AAC50508.1; -
DR EMBL: BC016174; AAH16174.1; -
DR PDB: 1QBH; 20-OCT-99.
DR Genew: HGNC:590; BIRC2.
DR MIM: 601721; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; BIR_REPEAT_1; 3.
DR PROSITE: PS01282; BIR_REPEAT_2; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; zf_RING_1; FALSE_NEG.
DR PROSITE: PS50089; zf_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat; 3D-structure.
DR KW REPEAT 46 113 BIR 1.
DR REPEAT 184 250 BIR 2.
DR REPEAT 269 336 BIR 3.
DR DOMAIN 453 543 CARD.
DR ZN_FING 571 606 CARD.
DR FT CONFLICT 157 157 S -> P (IN REF. 2).
DR FT CONFLICT 308 308 C -> G (IN REF. 2).
DR FT CONFLICT 414 414 Q -> L (IN REF. 2).
DR FT CONFLICT 514 514 L -> W (IN REF. 2).
DR FT CONFLICT 514 514 L -> W (IN REF. 2).
DR SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 100.0%; Score 295; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 5.6e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PEQLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVWHAKEPRCE 48
Db 287 PEQLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVWHAKEPRCE 334

RESULT 2
BIR_CHICK
ID BIR_CHICK STANDARD; PRT; 611 AA.
AC 090660;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (inhibitor of T cell apoptosis
protein).
```

```
GN ITA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=97101112; PubMed=8945639;
RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "ITA, a vertebrate homologue of IAP that is expressed in T
RT lymphocytes.";
RL DNA Cell Biol. 15:981-988(1996).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U27466; AAB48118.1; -
DR HSSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; BIR_REPEAT_1; 3.
DR PROSITE: PS01282; BIR_REPEAT_2; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; zf_RING_1; FALSE_NEG.
DR PROSITE: PS50089; zf_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat; Nuclear protein.
DR KW REPEAT 30 97 BIR 1.
DR REPEAT 176 242 BIR 2.
DR REPEAT 262 329 BIR 3.
DR DOMAIN 446 536 CARD.
DR ZN_FING 564 599 RING-TYPE.
DR SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;

Query Match 98.3%; Score 290; DB 1; Length 611;
Best Local Similarity 95.8%; Pred. No. 2.3e-28;
Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEQLADAGFYVGRNDVKCFCCDGLRCWESGDDPWVWHAKEPRCE 48
Db 280 PEQLADAGFYVGRNDVKCFCCDGLRCWESGDDPWVWHAKEPRCE 327

RESULT 3
PIAP_PIG
ID PIAP_PIG STANDARD; PRT; 358 AA.
AC 062640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
```

```

DE Putative inhibitor of apoptosis.
GN PIAP.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98162622; PubMed=9501011;
RA Stehlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
RL protein (Iap) family member is regulated by NF-kappa B.";
RI Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1 SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1 SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1 SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-----
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-----
DR EMBL: U79142; AAC39171.1; -.
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnfRING.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PSS0209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
KW REPEAT
FT REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT DOMAIN 193 283 CARD.
FT ZN_FING 311 346 RING-TYPE.
SQ SEQUENCE 358 AA; 40977 MW; EB226BFA9A6190A4 CRC64;

Query Match          95.6%; Score 282; DB 1; Length 358;
Best Local Similarity 93.8%; Pred. No. 1.3e-27;
Matches 45; Conservative 2; Mismatches 1. Indels 0; Gaps 0;

OY      1 PEGLASAGFYVGRNDVKFCPCDGGLRCWESGDDPWVEHAKIFRCE 48
       |||||l|||||l:l:|||||l|||||l|||||l|||||l|||||l
Db    108 PEOLASAGFYVMGHSDVDKCFCCDGGLRCWESGDDPWVEHAKIFRCE 155

RESULT 4
BIR2_HUMAN
AC Q13489; O16628; Q9UP46; Q9HC27; STANDARD; PRT; 604 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral iAP repeat-containing protein 1 (Inhibitor of apoptosis
DE protein 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF signaling complex
DE protein 1) (IAP homolog C).
DE BIRC2 OR API1 OR IAPI OR MTHC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=85448810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RL to baculoviral inhibitor of apoptosis proteins.";
RN Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Fatahant R., McLean M., Ikega J., Mackenzie A., Kornelut R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RL family of IAP genes.";
RN Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RL function to inhibit apoptosis and/or bind tumor necrosis factor
RN receptor-associated factors.";
RN Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99252096; PubMed=10233894;
RA Horrevorts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RL factor-alpha in vitro are expressed in atherosclerotic lesions,
RN including inhibitor of apoptosis protein-1, stannin, and two novel
RN genes.";
RN Blood 93:3418-3431(1999).
RN [5]
RP SEQUENCE OF 362-441 FROM N.A.
RX MEDLINE=20519161; PubMed=11066071;
RA Baens M., Steyls A., Dierlam J., De Wolf-peeters C., Marynen P.;
RT "Structure of the MALT gene and molecular characterization of the
RL genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone
RN B-cell lymphomas of MALT type.";
RN Genes Chromosomes Cancer 29:281-291(2000).
RN [1]
RP FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
RX WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC [1]
RP SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC [1]
RP SUBCELLULAR LOCATION: cytoplasmic (Potential).
CC [1]
RP TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC [1]
RP DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC tissue). This translocation is found in approximately 50% of
CC cytogenetically abnormal low-grade MALT lymphoma and involves
CC MALT1 and BIRC2.
CC [1]
RP SIMILARITY: BELONGS TO THE IAP FAMILY.
CC [1]
RP SIMILARITY: CONTAINS 3 BIR REPEATS.
CC [1]
RP SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC [1]
RP SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC [1]
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CC or send an email to license@isb-sib.ch).
CC EMBL; L49432; MAC41943.1; -

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DR EMBL: U45878; AAC50371.1; -
DR EMBL: U37546; AAC50507.1; -
DR EMBL: AF070674; AAC8323.1; -
DR EMBL: AF178945; AAC09369.1; -
DR HSSP: Q13490; IQBH.
DR Genew: HGNC:591; BIRC3.
DR MIM: 601712; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.
KW REPEAT
FT REPEAT 29 96 BIR 1.
FT REPEAT 169 235 BIR 2.
FT REPEAT 255 322 BIR 3.
FT DOMAIN 439 529 CARD.
FT ZN_FING 557 592 CARD.
FT SITE 442 443 RING-TYPE.
FT BIRC2-MULTI.
FT CONFLICT 18 18 N -> Y (IN REF. 4).
FT CONFLICT 119 119 N -> H (IN REF. 2).
FT CONFLICT 153 153 D -> E (IN REF. 2).
FT CONFLICT 163 163 H -> P (IN REF. 2).
FT CONFLICT 165 165 A -> P (IN REF. 2).
FT CONFLICT 191 191 K -> R (IN REF. 2).
FT CONFLICT 364 364 F -> L (IN REF. 2).
FT CONFLICT 552 552 Q -> P (IN REF. 2).
SQ SEQUENCE 604 AA; 68371 MW; 8581A0B9A8A4A7 CRC64;

Query Match          95.6%; Score 282; DB 1; Length 604;
Best Local Similarity 93.8%; Pred. No. 2.2e-27;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHAKWPRCE 48
Db 273 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHAKWPRCE 320

RESULT 5
BIR2_MOUSE
ID BIR2_MOUSE STANDARD; PRT; 612 AA.
AC Q62210; O08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
  protein 2) (MIAP2) (MIAP-2).
GN BIRC3 OR API2 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
  to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
```

```
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
  1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
  WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
  FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
  NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
  inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
  LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: L49433; AAC42078.1; -
DR EMBL: U88909; AAC53532.1; -
DR HSSP: Q13490; IQBH.
DR MGD; MGI:1197009; Birc3.
DR InterPro: IPR001370; Birc3.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
KW REPEAT
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match          95.6%; Score 282; DB 1; Length 612;
Best Local Similarity 93.8%; Pred. No. 2.2e-27;
Matches 45; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHAKWPRCE 48
Db 280 PEOLASAGFYVGRNDVKCFCCDGLRCWESGDDPWVHAHAKWPRCE 327

RESULT 6
BIR2_MOUSE
ID BIR2_MOUSE STANDARD; PRT; 600 AA.
AC Q08863;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
  protein 1) (MIAP1) (MIAP-1).
GN BIRC2 OR API1 OR IAP1.
OS Mus musculus (Mouse).
```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE-98110590; PubMed-9441758;
 RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
 RT "Genomic characterization of the mouse inhibitor of apoptosis protein
 1 and 2 genes.";
 RL Genomics 46:495-503(1997).
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
 CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
 CC inhibit apoptotic suppressor activity (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC -----
 DR EMBL: U88908; AAC53531.1; -
 DR HSSP: Q13490; IOBH.
 DR MGD: MGI:1197007; Birc2.
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 3.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Apoptosis; zinc-finger; Repeat.
 FT REPEAT 27 94 BIR 1.
 FT REPEAT 167 233 BIR 2.
 FT REPEAT 253 320 BIR 3.
 FT DOMAIN 436 525 CARD.
 FT ZN_FING 553 588 RING-TYPE.
 SQ SEQUENCE 600 AA; 67198 MW; AD7F73E6849317D1 CRC64;
 Query Match 90.8%; Score 268; DB 1; Length 600;
 Best Local Similarity 89.4%; Pred. No. 1.2e-25;
 Matches 42; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

GN IAP3 OR IAP.
 OS Orygia pseudotsugata multicausid polyhedrosis virus (OpMVV).
 CC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 CC Nucleopolyhedrovirus.
 CC NCBI_Taxid-164623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94187094; PubMed-8139034;
 RA Birnbaum M.J., Clem R.J., Miller L.K.;
 RT "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
 RT encoding a polypeptide with Cys/His sequence motifs.";
 RL J. Virol. 68:2521-2528(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97271300; PubMed-9126251;
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 RA Rohmann G.F.;
 RT "The sequence of the Orygia pseudotsugata multicausid nuclear
 RT polyhedrosis virus genome.";
 RL Virology 229:381-399(1997).
 CC -1- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY
 CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.
 CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC -----
 DR EMBL: L22564; AAB02610.1; -
 DR HSSP: U75930; AAC59034.1; -
 DR MGD: MGI:1197007; Birc2.
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00653; BIR; 2.
 DR SMART: SM00238; BIR; 2.
 DR SMART: SM00114; CARD; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS50143; BIR_REPEAT_2; 2.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Apoptosis; zinc-finger; Repeat.
 FT REPEAT 18 84 BIR 1.
 FT REPEAT 111 178 BIR 2.
 FT ZN_FING 221 256 RING-TYPE.
 SQ SEQUENCE 268 AA; 30076 MW; DF89175FDE85A708 CRC64;
 Query Match 67.1%; Score 198; DB 1; Length 268;
 Best Local Similarity 60.4%; Pred. No. 2.3e-17;
 Matches 29; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 PEGLASAGFYVGRNDVKFCFCCDGLRCWESGDDPWVHAHAKMPRCE 48
 Db 129 PEGLASAGFYVGRNDVKFCFCCDGLRCWESGDDPWVHAHAKMPRCE 176

RESULT 8
 ID BIR7_HUMAN STANDARD; PRT; 298 AA.
 AC 096CA5; 09H2A8; 09HAP7; 09BOV0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 7 (Kidney inhibitor of
 DE apoptosis protein) (KIAP) (Melanoma inhibitor of apoptosis protein)
 DE (ML-IAP) (Livin).
 GN BIRC7 OR KIAP OR ML-IAP OR LIVIN.
 OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fetal kidney;
RX PubMed=11162435;
RA Lin J.-H., Deng G., Huang Q., Morser J.;
RT "KIAP, a novel member of the inhibitor of apoptosis protein family.";
RL Biochem. Biophys. Res. Commun. 279:820-831(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Melanoma;
RX PubMed=11322947;
RA Ashhab Y., Allan A., Pollack A., Panet A., Yehuda D.B.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
RL different biological properties and tissue distribution pattern.";
RN FEBS Lett. 495:56-60(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Kidney;
RX PubMed=11024045;
RA Kasof G.M., Gomes B.C.;
RT "Livin, a novel inhibitor of apoptosis protein family member.";
RL J. Biol. Chem. 276:3238-3246(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
RX DELINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RN Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Frazer A., French L., Garner P.,
RA Grafham D.V., Griffiths J.C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.M., Johnson S.,
RA Levasaialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.D., McConachie L.J., McKay K., McMurtry A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symmons N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Skin;
RX Strausberg R.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP FUNCTION, AND MUTAGENESIS OF GLU-87; GLU-88; CYS-124; ASP-120 AND
RN ASP-138.
RX PubMed=11084335;
RA Vucic D., Stennicke H.R., Pisabarro M.T., Salvesen G.S., Dixit V.M.;
RT "ML-IAP, a novel inhibitor of apoptosis that is preferentially
RN expressed in human melanomas.";
RL Curr. Biol. 10:1359-1366(2000).
RN [7]
RP INTERACTION WITH SMAC.
RX PubMed=11801603;
RA Vucic D., Deshayes K., Ackerly H., Pisabarro M.T., Kadkodayan S.,
RA Fairbrother W.J., Dixit V.M.;

RT "SMAC negatively regulates the anti-apoptotic activity of melanoma
RT inhibitor of apoptosis (ML-IAP).";
RL J. Biol. Chem. 277:12275-12279(2002).
RN [8]
RP ACTIVATION OF MAP KINASES.
RX PubMed-11865055;
RA Sanna M.G., da Silva Correia J., Duxreay O., Lee J., Nomoto K.,
Schrantz N., Devereaux Q.L., Ulevitch R.J.;
RT "IAP suppression of apoptosis involves distinct mechanisms: the
TNF1/TAK1 signaling cascade and caspase inhibition.";
RL Mol. Cell. Biol. 22:1754-1766(2002).
CC -1- FUNCTION: Protects against apoptosis induced by TNF or by chemical
agents such as adriamycin, etoposide or staurosporine. Suppression
of apoptosis is mediated by activation of MAPK8/JNK1, and possibly
also of MAPK9/JNK2. This activation depends on TAB1 and
NR2C2/TAK1. In vitro, inhibits caspase-3 and proteolytic
activation of pro-caspase-9. Isoform 1 blocks staurosporine-
induced apoptosis and isoform 2 blocks etoposide-induced
apoptosis.
CC -1- SUBUNIT: Binds to caspase-9. Interaction with SMAC via the BIR
domain disrupts binding to caspase-9 and apoptotic suppressor
activity. Interacts with TAB1. In vitro, interacts with caspase-3
and caspase-7 via its BIR domain.
CC -1- SUBCELLULAR LOCATION: Nuclear, and in a filamentous pattern
throughout the cytoplasm.
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms: 1/Livin beta, 2/Livin alpha
(shown here) and 3; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Very low levels or not detectable in most
adult tissues. Detected in adult heart, placenta, lung, lymph
node, spleen and ovary, and in several carcinoma cell lines
(isoforms 1 and 2). Isoform 2 (but not isoform 1) is detected in
fetal kidney, heart and spleen, and at lower levels in adult
brain, skeletal muscle and peripheral blood leukocytes.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).

DR EMBL: AF301009; AAG37878.1; -
DR EMBL: AJ309298; CAC37337.1; -
DR EMBL: AJ309298; CAC37338.1; -
DR EMBL: AF311388; AAG33622.1; -
DR EMBL: AL121827; CAC36111.1; -
DR EMBL: AL121827; CAC36112.1; -
DR EMBL: AL121827; CAC36113.1; ALF_INIT.
DR EMBL: BC014475; AAH14475.1; -
DR HSSP: Q13490; IOBH.
DR Genew: HGNC:13702; BIRC7.
DR MIM: 605737; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; znf_rlng.
DR Pfam: PF00653; BIR, 1.
DR Pfam: PF00097; zf-C3HC4, 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 1.
DR PROSITE: PS00518; zf_RING_1; 1.
DR PROSITE: PS50089; zf_RING_2; 1.
KW Apoptosis; zinc-finger; Alternative splicing.
FT REPEAT 90 155
FT ZN_FING 252 286
FT DOMAIN 64 69
FT VARSPIC 1 149

MGPKDSAKCLHKGPPQSHWAAGDPTQERCGPRSLGSPVLG
LDTGRAMDVAHQIILGOLRLTEEEEBGAGATLSRGPAP
GMGSEELRLASFMDPLTAEPBELLAAGFFHTGHODKVR
CFICYGLQSWKRGDDPWTETAAKWP -> MFLPMDPEAP
WRLHSSBPRLCPRALGGGRGPNPDRGSGGLKQTVGAL

```
FT  VARSPLIC 216 233 NPNILMLGIC (IN ISOFORM 3).
FT  MUTAGEN 87 88 MISSING (IN ISOFORM 1).
FT  MUTAGEN 120 120 EE->AA: NO CHANGE IN SMAC INTERACTION AND
FT  MUTAGEN 124 124 ANTI-APOPTOTIC ACTIVITY.
FT  MUTAGEN 138 138 D->A: ABOLISHES INHIBITION OF CASPASES,
SMAC BINDING AND ANTI-APOPTOTIC ACTIVITY.
FT  MUTAGEN 138 138 C->A: ABOLISHES INHIBITION OF CASPASES,
AND ANTI-APOPTOTIC ACTIVITY.
FT  MUTAGEN 138 138 D->A: ABOLISHES INHIBITION OF CASPASES,
SMAC BINDING AND ANTI-APOPTOTIC ACTIVITY.
FT  CONFLICT 223 223 E -> Q (IN REF. 5).
SQ  SEQUENCE 298 AA; 32798 MW; B2EAAE531BEC101 CRC64;

Query Match
Best Local Similarity 66.1%; Score 195; DB 1; Length 298;
Matches 30; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 PEOIASAGFYVGRNDYKCFCCDGLRCWESGDDPVEVHAKEPPE 48
Db 105 PELLAAAGFEHTGHQDKVRCFCYGLQSKWRGDDPVEVHAKEPPE 152

RESULT 9
BIR_MOUSE STANDARD; PRT; 1403 AA.
ID BIR_MOUSE
AC 09JIB6; P81704; 009122; 009121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1f (Neuronal apoptosis
inhibitory protein 6).
GN BIRC1F OR NAIP6 OR NAIP-RS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20414747; PubMed-10958627;
RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
RN [2]
RP SEQUENCE OF 82-168 FROM N.A.
RC STRAIN-129/SVJ;
RX MEDLINE-97131520; PubMed-8975718;
RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
within the Lgl1 critical interval and contains multiple copies of Naip
exon 5.";
RL Genomics 38:405-417(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL; AF242431; AAF82751.1; -.
DR EMBL; U66327; AAC52975.1; -.
DR HSSP; Q13490; 1QBH.
DR MGD; MGI:1298222; Birc1f.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR. 3.
DR SMART; SM00238; BIR. 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
```

```
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1403 AA; 159823 MW; 9D4912503358C4E9 CRC64;

Query Match
Best Local Similarity 63.4%; Score 187; DB 1; Length 1403;
Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 PEOIASAGFYVGRNDYKCFCCDGLRCWESGDDPVEVHAKEPPE 48
Db 178 PRAISAAGFYVGRNDYKCFCCDGLRCWESGDDPVEVHAKEPPE 225

RESULT 10
BIR_MOUSE STANDARD; PRT; 1402 AA.
ID BIR_MOUSE
AC 09JIB3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
inhibitory protein 7).
GN BIRC1G OR NAIP7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20414747; PubMed-10958627;
RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL; AF242433; AAF82749.1; -.
DR HSSP; Q13490; 1QBH.
DR MGD; MGI:1858256; Birc1g.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR. 3.
DR SMART; SM00238; BIR. 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1402 AA; 159662 MW; C1DFEBA359893E0D CRC64;

Query Match
Best Local Similarity 63.1%; Score 186; DB 1; Length 1402;
Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 PEOIASAGFYVGRNDYKCFCCDGLRCWESGDDPVEVHAKEPPE 48
Db 1 PEOIASAGFYVGRNDYKCFCCDGLRCWESGDDPVEVHAKEPPE 48
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DB 178 PRVLSAGFVFTGKRDVOCFSCGSLGNWEEGDDPWKEHAKWPKCE 225

RESULT 11

BIR_MOUSE

ID BIR_MOUSE STANDARD; PRT: 1403 AA.

AC 09QWKS; 09R017; 09JIB5;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Baculoviral IAP repeat-containing protein 1a (Neuronal apoptosis inhibitory protein 1).

GN BIRCL1 OR NAIP1 OR NAIP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RA Varaghi Z., Korneluk R.G., Mackenzie A.E.;

RT "Cloning and characterization of the multiple copies of the murine homologue of NAIP (neuronal apoptosis inhibitory protein).";

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE FROM N.A.

RX MEDLINE=99431676; PubMed=10501978;

RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;

RT "The mouse Naip gene cluster on chromosome 13 encodes several distinct functional transcripts.";

RL Mamm. Genome 10:1032-1035(1999).

[3]

SEQUENCE FROM N.A.

RX MEDLINE=20414747; PubMed=10958627;

RA Endrizzi M.G., Hadimoto V., Growney J.D., Miller W., Dietrich W.F.;

RT "Genomic sequence analysis of the mouse Naip gene array.";

RL Genome Res. 10:1095-1102(2000).

-1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.

-1- SIMILARITY: CONTAINS 3 BIR REPEATS.

-1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.

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DR EMBL; AF007769; AAB69223.1; -

DR EMBL; AF135491; AAD56763.1; -

DR EMBL; AF242432; AAF62752.1; -

DR HSSP; Q13490; 10BH.

DR MGD; MGI:1298223; Birc1a.

DR InterPro; IPR001370; BIR.

DR Pfam; PF00653; BIR; 3.

DR SMART; SM00238; BIR; 3.

DR PROSITE; PS01282; BIR_REPEAT_1; 1.

DR PROSITE; PS50143; BIR_REPEAT_2; 3.

DR PROSITE; PS50837; NACHT; 1.

KW Apoptosis; Repeat; Multigene family.

FT REPEAT 60 127 BIR 1.

FT REPEAT 159 227 BIR 2.

FT REPEAT 278 345 BIR 3.

FT DOMAIN 464 758 NACHT.

FT CONFLICT 343 343 I -> V (IN REF. 2).

FT CONFLICT 359 359 L -> Q (IN REF. 2).

FT CONFLICT 624 624 E -> K (IN REF. 2).

FT CONFLICT 1092 1092 D -> E (IN REF. 3).

FT CONFLICT 1116 1116 D -> N (IN REF. 3).

FT CONFLICT 1123 1123 G -> R (IN REF. 3).

FT CONFLICT 1129 1129 L -> H (IN REF. 1).

FT CONFLICT 1140 1140 T -> M (IN REF. 2).

FT CONFLICT 1269 1269 A -> V (IN REF. 3).

SEQ SEQUENCE 1403 AA; 158692 MW; B31630259595EE67 CRC64;

Query Match

Best Local Similarity 63.1%; Score 186; DB 1; Length 1403;

Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 PEGLASAGFYVGRNDVKFCDCGGLRCWESGDDPWKEHAKWPKCE 48

DB 178 PRVLSAGFVFTGKRDVOCFSCGSLGNWEEGDDPWKEHAKWPKCE 225

RESULT 12

BIR_MOUSE

ID BIR_MOUSE STANDARD; PRT: 1403 AA.

AC 09R016; 09R029; P81703; 009122; 009121;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis inhibitory protein 5).

GN BIRCL1 OR NAIP5 OR NAIP-RS3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RX MEDLINE=99431676; PubMed=10501978;

RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;

RT "The mouse Naip gene cluster on chromosome 13 encodes several distinct functional transcripts.";

RL Mamm. Genome 10:1032-1035(1999).

[2]

SEQUENCE FROM N.A.

RX STRAIN=129/SV;

RA MEDLINE=99417674; PubMed=10486205;

RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B., Kunkel L.M., Miller W., Dietrich W.F.;

RT "Comparative sequence analysis of the mouse and human Lgln1/SMA interval.";

RL Genomics 60:137-151(1999).

[3]

SEQUENCE OF 82-168 FROM N.A.

RP STRAIN=129/SV;

RX MEDLINE=97131520; PubMed=8975718;

RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H., Kunkel L.M., Dietrich W.F.;

RT "The mouse region syntenic for human spinal muscular atrophy lies within the Lgln1 critical interval and contains multiple copies of Naip exon 5.";

RL Genomics 38:405-417(1996).

-1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.

-1- SIMILARITY: CONTAINS 3 BIR REPEATS.

-1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.

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DR EMBL; AF135492; AAD56764.1; -

DR EMBL; AF131205; AAD56760.1; -

DR EMBL; U66326; AAC52974.1; -

DR HSSP; Q13490; 10BH.

DR MGD; MGI:1298220; Birc1e.

DR InterPro; IPR001370; BIR.

DR Pfam; PF00653; BIR; 3.

DR SMART; SM00238; BIR; 3.

DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50837; NACHT; 1.
 KW Apoptosis; Repeat; Multigene family.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.
 FT REPEAT 278 345 BIR 3.
 FT DOMAIN 464 759 NACHT.
 FT CONFLICT 92 92 K -> R (IN REF. 1).
 FT CONFLICT 144 144 S -> R (IN REF. 1).
 FT CONFLICT 242 242 S -> G (IN REF. 2).
 FT CONFLICT 472 472 T -> A (IN REF. 2).
 FT CONFLICT 516 516 A -> D (IN REF. 2).
 FT CONFLICT 521 521 A -> T (IN REF. 2).
 FT CONFLICT 533 533 V -> A (IN REF. 2).
 FT CONFLICT 538 538 S -> I (IN REF. 2).
 FT CONFLICT 1092 1092 E -> D (IN REF. 2).
 FT CONFLICT 1129 1129 H -> L (IN REF. 2).
 FT CONFLICT 1137 1137 R -> Q (IN REF. 2).
 FT CONFLICT 1242 1242 V -> I (IN REF. 2).
 FT CONFLICT 1276 1276 D -> N (IN REF. 2).
 SQ SEQUENCE 1403 AA; 159695 MW; B27F645043BCEC42 CRC64;

Query Match Best Local Similarity 63.1%; Score 186; DB 1; Length 1403;
 Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

OY 1 PEOALSAGFYVGRNDVKFCDCDGLRCWESGDDPWVHAKEPKE 48
 DB 178 PVLASAGFYVGRNDVKFCDCDGLRCWESGDDPWVHAKEPKE 225

RESULT 13
 BIRB_MOUSE
 ID BIRB_MOUSE STANDARD; PRT; 1447 AA.
 AC 090UK4; Q9R030; O09124;
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Baculoviral IAP repeat-containing protein 1b (Neuronal apoptosis
 inhibitory protein 2).
 GN BIRC1B OR NAIP2 OR NAIP-RS6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99431676; PubMed-10501978;
 RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
 RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
 functional transcripts."
 RL Mamm. Genome 10:1032-1035(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99315342; PubMed-10384056;
 RA Yaraqhi Z., Diez E., Gros P., Mackenzie A.;
 RT "cDNA cloning and the 5'genomic organization of Naip2, a candidate
 gene for murine Legionella resistance."
 RL Mamm. Genome 10:761-763(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN-129/SV;
 MEDLINE-99417674; PubMed-10486205;
 RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
 RA Kunkel L.M., Miller W., Dietrich W.F.;
 RT "Comparative sequence analysis of the mouse and human Igml/SMa
 interval."
 RL Genomics 60:137-151(1999).
 RN [4]
 RP SEQUENCE OF 82-168 FROM N.A.
 RX STRAIN-129/SV;
 MEDLINE-97131520; PubMed-8975718;
 RX

RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
 RA Kunkel L.M., Dietrich W.F.;
 RT "The mouse region syntenic for human spinal muscular atrophy lies
 within the Igml critical interval and contains multiple copies of Naip
 exon 5."
 RL Genomics 38:405-417(1996).
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 SIGNALS.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
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 or send an email to license@isb-sib.ch).

DR EMBL; AF135489; AAD56761.1; -
 DR EMBL; AF135490; AAD56762.1; -
 DR EMBL; AF102871; AAC73002.1; -
 DR EMBL; AF131205; AAD56759.1; -
 DR EMBL; U66329; AAC52977.1; -
 DR HSSP; Q13490; 1QBH.
 DR MGI; MGI:1298226; Birc1b.
 DR InterPro; IPR001370; BIR.
 DR Pfam; PF00653; BIR; 3.
 DR SMART; SM00238; BIR; 3.
 DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50837; NACHT; 1.
 KW Apoptosis; Repeat; Multigene family.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.
 FT REPEAT 278 345 BIR 3.
 FT DOMAIN 508 802 NACHT.
 FT CONFLICT 377 377 D -> G (IN REF. 3).
 FT CONFLICT 403 403 L -> F (IN REF. 3).
 FT CONFLICT 478 478 L -> I (IN REF. 3).
 FT CONFLICT 540 540 N -> Y (IN REF. 3).
 FT CONFLICT 862 862 K -> N (IN REF. 3).
 FT CONFLICT 1079 1080 SD -> FN (IN REF. 3).
 FT CONFLICT 1089 1089 R -> C (IN REF. 3).
 FT CONFLICT 1115 1115 K -> E (IN REF. 3).
 FT CONFLICT 1122 1122 T -> A (IN REF. 3).
 FT CONFLICT 1136 1136 D -> E (IN REF. 3).
 FT CONFLICT 1157 1157 S -> G (IN REF. 3).
 FT CONFLICT 1167 1167 G -> R (IN REF. 3).
 FT CONFLICT 1271 1271 F -> C (IN REF. 3).
 SQ SEQUENCE 1447 AA; 164033 MW; 9EF6CA73BAE60A2 CRC64;

Query Match Best Local Similarity 62.0%; Score 183; DB 1; Length 1447;
 Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

OY 1 PEOALSAGFYVGRNDVKFCDCDGLRCWESGDDPWVHAKEPKE 48
 DB 178 PVLASAGFYVGRNDVKFCDCDGLRCWESGDDPWVHAKEPKE 225

RESULT 14
 IAP_GVCP
 ID IAP_GVCP STANDARD; PRT; 275 AA.
 AC P41436;
 DT 01-NOV-1995 (Rel. 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Apoptosis inhibitor IAP.
 GN IAP.
 OS Cydia pomonella granulosis virus (CpGV) (Cydia pomonella
 granulovirus).
 OS Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OC

```

OX NCBI_TaxID=28289;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1;
RX MEDLINE=93188168; PubMed=8445726;
RA Crook N.E., Clem R.J., Miller L.K.;
RT "An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif."
RL J. Virol. 67:2168-2174(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mexican;
RA Kang W.K., Crook N.E., Winstanley D., O'Reilly D.R.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY PREVENTING VIRAL STIMULATION OF APOPTOSIS.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U53466; AAB39098.1; -
DR HSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
KW REPEAT 73
FT REPEAT 108 175 BIR 1.
FT ZN_FING 228 263 RING-TYPE.
SQ SEQUENCE 275 AA; 31290 MW; 8460544869CAD60 CRC64;

Query Match 61.7%; Score 182; DB 1; Length 275;
Best Local Similarity 59.6%; Pred. No. 2, 2e-15;
Matches 28; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 PEOLASAGFYVGRNDVVKFCDCGRLCWESGDDPWEHAKIFPRC 47
Db 126 PEQKADAGFFYGTGDKTKCYCDGGLKDWEPDVPWEQHVWPRC 172

RESULT 15
BIRL_HUMAN
ID BIRL_HUMAN STANDARD; PRT; 1403 AA.
AC Q13075; Q13730; Q99796; Q75857;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis inhibitory protein).
DE BIRCL OR NAIP.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95112344; PubMed=7813013;
RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yaraqti Z., Farahani R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,

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RA Salih M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O.,
RA de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;
RT "The gene for neuronal apoptosis inhibitory protein is partially deleted in individuals with spinal muscular atrophy."
RL Cell 80:167-178(1995).
RN [2]
RP SEQUENCE FROM N.A., AND REVISIONS.
RC TISSUE=Brain;
RX MEDLINE=98163755; PubMed=9503025;
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R., Xuan J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G., Mackenzie A.E.;
RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular atrophy candidate genes SMN and NAIP."
RL Genomics 48:121-127(1998).
RN [3]
RP SEQUENCE OF 386-623 FROM N.A.
RA der Steege G., Draaijers T.G., Grootscholten P.M., Oslinga J., Anzevino R., Velona I., Brane C., Scheffer H., van Ommen G.J.B., Buys C.H.C.M.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 222-1403 FROM N.A.
RA Jones K., Graves T., McPherson J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes."
RL Nature 379:349-353(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN SPINAL CORD.
CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE I). SMAS ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I (WERNIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE III (WOLFFHART-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000 NEWBORNS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U19251; AAC52045.1; -
DR EMBL: U80017; AAC52047.1; -
DR EMBL: U21913; AAA64504.1; -
DR EMBL: AC005031; AAC62261.1; -
DR HSP: Q13490; IOBH.
DR GeneW: HGNC:7634; BIRCL.
DR MIM: 600355; -
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50837; NACHT; 1.
KW Apoptosis; Repeat.

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FT	REPEAT	60	127	BIR 1.
FT	REPEAT	159	227	BIR 2.
FT	REPEAT	278	345	BIR 3.
FT	DOMAIN	464	758	NACHT.
FT	CONFLICT	222	223	PK -> YR (IN REF. 4).
FT	CONFLICT	386	387	VP -> ST (IN REF. 3).
FT	CONFLICT	535	535	M -> V (IN REF. 3).
FT	CONFLICT	553	553	Y -> H (IN REF. 3).
FT	CONFLICT	1228	1231	MISSING (IN REF. 4).
SO	SEQUENCE	1403	AA; 159613	MM; 565034C154DA5E64
				CRC64;

Query Match	60.3%;	Score 178;	DB 1;	Length 1403;
Best Local Similarity	60.4%;	Pred. No. 3.1e-14;		
Matches 29; Conservative	5;	Mismatches 14;	Indels 0;	Gaps 0;

Dp Qy

1 PEGLASAGYYVGRNDYKCCPCDDGLRCMESGDDPWTENAKWPFKE 48
| : | | : | : | | | | | | | | | | | |
178 PCVISAEAGVFETGKODIVQCFSCGGCLGNMECGDDPWTEHAKWPFKE 225

Search completed: May 5, 2003, 16:02:48
Job time : 3.99078 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 3.73848 Seconds

(without alignments)
432.866 Million cell updates/sec

Title: US-08-569-749-6

Perfect score: 308

Sequence: 1 CELYRMSTYSTFPAGVPVSE.....KVKFCGGLMDNMRGDS

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pcp:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pcp:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pcp:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pcp:*
5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pcp:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308	100.0	55	4	US-08-569-749-6
2	308	100.0	55	5	PCr-US96-12860-6
3	308	100.0	604	2	US-08-511-485-6
4	308	100.0	604	3	US-09-212-971-6
5	308	100.0	604	4	US-08-800-929A-6
6	308	100.0	604	4	US-08-569-749-4
7	308	100.0	604	4	US-09-617-053A-6
8	308	100.0	604	5	PCr-US96-12860-4
9	301	97.7	55	4	US-08-569-749-5
10	301	97.7	55	5	PCr-US96-12860-5
11	301	97.7	618	2	US-08-511-485-8
12	301	97.7	618	3	US-09-212-971-8
13	301	97.7	618	4	US-08-800-929A-8
14	301	97.7	618	4	US-08-569-749-2
15	301	97.7	618	4	US-09-617-053A-8
16	301	97.7	618	4	US-09-069-023-29
17	301	97.7	618	5	PCr-US96-12860-2
18	299	97.1	68	2	US-08-511-485-18
19	294	95.5	612	3	US-09-212-971-14
20	294	95.5	612	4	US-08-800-929A-14
21	294	95.5	612	4	US-08-569-749-14
22	294	95.5	612	4	US-09-617-053A-14
23	294	95.5	612	5	PCr-US96-12860-14
24	292	94.8	68	2	US-08-511-485-19
25	287	93.2	600	3	US-09-212-971-12
26	287	93.2	600	4	US-08-800-929A-12
27	287	93.2	600	4	US-09-617-053A-12

28	158	51.3	68	2	US-08-511-485-17	Sequence 17, Appl
29	158	51.3	497	2	US-08-511-485-4	Sequence 4, Appl
30	158	51.3	497	3	US-09-212-971-4	Sequence 4, Appl
31	158	51.3	497	4	US-08-800-929A-4	Sequence 4, Appl
32	158	51.3	497	4	US-09-617-053A-4	Sequence 4, Appl
33	152	49.4	68	2	US-08-511-485-16	Sequence 16, Appl
34	152	49.4	496	2	US-08-511-485-10	Sequence 10, Appl
35	152	49.4	496	3	US-09-212-971-10	Sequence 10, Appl
36	152	49.4	496	4	US-08-800-929A-10	Sequence 10, Appl
37	152	49.4	496	4	US-09-617-053A-10	Sequence 10, Appl
38	151	49.0	438	5	PCr-US96-05922A-2	Sequence 2, Appl
39	139	45.1	68	2	US-08-511-485-27	Sequence 27, Appl
40	134	43.5	68	2	US-08-511-485-26	Sequence 26, Appl
41	133	43.2	68	2	US-08-511-485-28	Sequence 28, Appl
42	133	43.2	268	3	US-08-836-134-22	Sequence 22, Appl
43	133	43.2	268	4	US-09-493-784-22	Sequence 22, Appl
44	131	42.5	68	2	US-08-511-485-21	Sequence 21, Appl
45	129	41.9	68	2	US-08-511-485-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-569-749-6
Sequence 6, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-6

Query Match 100.0%; Score 308; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.9e-37;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDVKFCGGLMDNMRGDS 55
DB 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDVKFCGGLMDNMRGDS 55

RESULT 2
PCT-US96-12860-6
Sequence 6, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-6

Query Match 100.0%; Score 308; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.9e-37;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CELYRMSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 55

RESULT 3
US-08-511-485-6
Sequence 6, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-6

Query Match 100.0%; Score 308; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 55
DB 28 CELYRMSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 82

RESULT 4
US-09-212-971-6
Sequence 6, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 604
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-6

Query Match 100.0%; Score 308; DB 3; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 55
DB 28 CELYRMSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 82

RESULT 5
US-08-800-929A-6

Sequence 6, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-6

Query Match 100.0%; Score 308; DB 4; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGMLDNMKRGDSP 55
DB 28 CELYRMSTSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGMLDNMKRGDSP 82

RESULT 6
US-08-569-749-4
Sequence 4, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FIEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-4

Query Match 100.0%; Score 308; DB 4; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGMLDNMKRGDSP 55
DB 28 CELYRMSTSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGMLDNMKRGDSP 82

RESULT 7
US-09-617-053A-6
Sequence 6, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 604
TYPE: PRT
ORGANISM: Homo sapiens
US-09-617-053A-6

Query Match 100.0%; Score 308; DB 4; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGMLDNMKRGDSP 55
DB 28 CELYRMSTSTFPAGVPSERSLARAGFYTTGVNDKVKCFCCGMLDNMKRGDSP 82

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RESULT 8
PCT-US96-12860-4
; Sequence 4, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12860-4

Query Match          100.0%; Score 308; DB 5; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKRDSP 55
Db 28 CELYRMSTYTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKRDSP 82

RESULT 9
US-08-569-749-5
; Sequence 5, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Goeddel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/569,749
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12860-5

Query Match          97.7%; Score 301; DB 4; Length 55;
Best Local Similarity 98.2%; Pred. No. 6.9e-36;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTYTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKRDSP 55
Db 1 CELYRMSTYTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKLDSP 55

RESULT 10
PCT-US96-12860-5
; Sequence 5, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12860-5

Query Match          97.7%; Score 301; DB 5; Length 55;
Best Local Similarity 98.2%; Pred. No. 6.9e-36;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-929A-8

Query Match 97.7%; Score 301; DB 4; Length 618;
Best Local Similarity 98.2%; Pred. No. 1.2e-34;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVKCCGGLMDNKRKGDSP 55
|||||
Db 45 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVKCCGGLMDNKRKGDSP 99

RESULT 14

US-08-569-749-2
Sequence 2, Application US/08569749
Patent No. 6187557

GENERAL INFORMATION:

APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 618 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-569-749-2

Query Match 97.7%; Score 301; DB 4; Length 618;
Best Local Similarity 98.2%; Pred. No. 1.2e-34;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVKCCGGLMDNKRKGDSP 55
|||||
Db 45 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVKCCGGLMDNKRKGDSP 99

RESULT 15

US-09-617-053A-8
Sequence 8, Application US/09617053A
Patent No. 6300492

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Iliston, Peter

APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-617-053A-8

Query Match 97.7%; Score 301; DB 4; Length 618;
Best Local Similarity 98.2%; Pred. No. 1.2e-34;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVKCCGGLMDNKRKGDSP 55
|||||
Db 45 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVKCCGGLMDNKRKGDSP 99

Search completed: May 5, 2003, 16:09:10
Job time : 4.73848 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:07 ; Search time 6.77995 Seconds

(without alignments)
699.970 Million cell updates/sec

Title: US-08-569-749-6

Perfect score: 308
Sequence: 1 CELYRMSTYSTFPAGVPVSE.....KVKCFCCGLMDNMRGSDSP 55

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308	100.0	604	9	US-09-201-936-6
2	308	100.0	604	10	US-09-974-592-6
3	301	97.7	306	10	US-09-778-927A-62
4	301	97.7	618	9	US-09-201-936-8
5	301	97.7	618	10	US-09-974-592-8
6	299	97.1	68	9	US-09-201-936-18
7	294	95.5	591	9	US-09-201-936-42
8	294	95.5	612	10	US-09-974-592-14
9	292	94.8	68	9	US-09-201-936-19
10	287	93.2	600	10	US-09-974-592-12
11	287	93.2	602	9	US-09-201-936-40
12	158	51.3	68	9	US-09-201-936-17
13	158	51.3	110	9	US-09-965-967-22
14	158	51.3	497	9	US-09-201-936-4
15	158	51.3	497	10	US-09-974-592-4
16	152	49.4	68	9	US-09-201-936-16
17	152	49.4	496	9	US-09-201-936-10
18	152	49.4	496	10	US-09-974-592-10
19	151	49.0	438	1	US-08-464-588-2

20	140	45.5	110	9	US-09-965-967-21	Sequence 21, Appl
21	139	45.1	68	9	US-09-201-936-27	Sequence 27, Appl
22	134	43.5	68	9	US-09-201-936-26	Sequence 26, Appl
23	133	43.2	68	9	US-09-201-936-28	Sequence 28, Appl
24	133	43.2	68	9	US-10-041-859-18	Sequence 18, Appl
25	133	43.2	172	9	US-10-041-859-12	Sequence 12, Appl
26	131	42.5	68	9	US-09-201-936-21	Sequence 21, Appl
27	129	41.9	68	9	US-09-201-936-20	Sequence 20, Appl
28	129	41.9	68	9	US-10-041-859-19	Sequence 19, Appl
29	129	41.9	109	9	US-09-965-967-30	Sequence 30, Appl
30	129	41.9	172	9	US-10-041-859-13	Sequence 13, Appl
31	128	41.6	1403	8	US-08-913-322-22	Sequence 22, Appl
32	128	41.6	1403	8	US-08-913-322-24	Sequence 24, Appl
33	121.5	39.4	67	9	US-09-201-936-22	Sequence 22, Appl
34	116	37.7	68	9	US-10-041-859-14	Sequence 14, Appl
35	116	37.7	172	9	US-10-041-859-8	Sequence 8, Appl
36	116	37.7	346	9	US-10-041-859-2	Sequence 2, Appl
37	115.5	37.5	67	9	US-09-201-936-23	Sequence 23, Appl
38	112	36.4	66	9	US-09-201-936-24	Sequence 24, Appl
39	112	36.4	66	9	US-09-201-936-25	Sequence 25, Appl
40	112	36.4	107	9	US-09-965-967-20	Sequence 20, Appl
41	112	36.4	278	9	US-09-964-899-39	Sequence 39, Appl
42	111.5	36.2	67	9	US-09-201-936-11	Sequence 11, Appl
43	111.5	36.2	109	9	US-09-965-967-19	Sequence 19, Appl
44	110	35.7	68	9	US-10-041-859-16	Sequence 16, Appl
45	110	35.7	172	9	US-10-041-859-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-201-936-6
; Sequence 6, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-201-936-6
Query Match 100.0%; Score 308; DB 9; Length 604;
Best Local Similarity 100.0%; Pred. No. 9.7e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTYGVNDVKCFCCGLMDNMRGSDSP 55
Db 28 CELYRMSTYSTFPAGVPVSESLARAGFYTYGVNDVKCFCCGLMDNMRGSDSP 82
RESULT 2
US-09-974-592-6
; Sequence 6, Application US/09974592

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; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-974-592-6
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Query Match          100.0%; Score 308; DB 10; Length 604;
Best Local Similarity 100.0%; Pred. No. 9.7e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 55
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DB 28 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 82
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RESULT 3
US-09-778-927A-62
; Sequence 62, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(306)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
; US-09-778-927A-62
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Query Match          97.7%; Score 301; DB 10; Length 306;
Best Local Similarity 98.2%; Pred. No. 3.9e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 55
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DB 45 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 99
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RESULT 4
US-09-201-936-8
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; Sequence 8, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-201-936-8
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Query Match          97.7%; Score 301; DB 9; Length 618;
Best Local Similarity 98.2%; Pred. No. 8.5e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 55
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DB 45 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 99
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RESULT 5
US-09-974-592-8
; Sequence 8, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-974-592-8
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Query Match          97.7%; Score 301; DB 10; Length 618;
Best Local Similarity 98.2%; Pred. No. 8.5e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 55
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DB 45 CELYRMSTYSTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 99
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RESULT 6

US-09-201-936-18
; Sequence 18, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-18

Query Match 97.1%; Score 299; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.3e-32;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCFCCGMLDNMKRGDSP 55
Db 1 ELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCFCCGMLDNMKRGDSP 54

RESULT 7

US-09-201-936-42
; Sequence 42, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-42

Query Match 95.5%; Score 294; DB 9; Length 591;
Best Local Similarity 94.5%; Pred. No. 6.9e-31;

Matches 52; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCFCCGMLDNMKRGDSP 55
Db 24 CELYRMSTYSAFPRGVPSERSLARAGFYTGVDKVKCFCCGMLDNMKRGDSP 78

RESULT 8

US-09-974-592-14
; Sequence 14, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-14

Query Match 95.5%; Score 294; DB 10; Length 612;
Best Local Similarity 94.5%; Pred. No. 7.2e-31;
Matches 52; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCFCCGMLDNMKRGDSP 55
Db 45 CELYRMSTYSAFPRGVPSERSLARAGFYTGVDKVKCFCCGMLDNMKRGDSP 99

RESULT 9

US-09-201-936-19
; Sequence 19, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-201-936-19

Query Match	94.8%;	Score 292;	DB 9;	length 68;
Best Local Similarity	98.1%;	Pred. No. 1.1e-31;		
Matches 53; Conservative	0;	Mismatches 1;	Indels 0;	Gaps .0;

Oy 2 ELYRSTYSTFPAGVPVSESLARAGFYYYGVNDKVKCCGGLMDNKKRGSP 55
| | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 1 ELYRSTYSTFPAGVPVSESLARAGFYYYGVNDKVKCCGGLMDNKKLGSP 54

RESULT 10
US-09-974-592-12

```

: APPLICANT: Korneluk, Robert G
: APPLICANT: Mackenzie, Alexander E
: APPLICANT: Liston, Peter
: APPLICANT: Baird, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Christine
: TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
: TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
: TITLE OF INVENTION: DISEASE
: FILE REFERENCE: 07891/009004
: CURRENT APPLICATION NUMBER: US/09/974,592
: CURRENT FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: US 09/617,053
: PRIOR FILING DATE: 2000-07-14
: PRIOR APPLICATION NUMBER: US 08/800,929
: PRIOR FILING DATE: 1997-02-13
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12
: LENGTH: 600
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-974-592-12

```

Query Match	93.28;	Score 287;	DB 10;	Length 600;
Best Local Similarity	90.98;	Pred. No. 6e-30;		
Matches 50; Conservative	2;	Mismatches 3;	Indels 0;	Gaps 0;

```
QY-      1 CELYRMSTYSIFPPAGVPSERSLARAGFYITGVNDKVKCFCCGLMLDNNKKRGSF 55  
          |||||::||| | |||||||::||| | |||||||::||| | |||||||::||| |  
Db       26 CELYRLSTYSAFPGRGVPVSERSLARAGFYITGVANDKVKECCGLMLDNNWKQGDSP 80
```

```

RESULT 11
US-09-201-936-40
; Sequence 40, Application US/09201936
; Publication NO. US20020187946A1
GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Bald, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ. ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0

```

```
; SEQ ID NO 40
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-40
```

Query Match	93.2%	Score 287	DB 9	Length 602
Best Local Similarity	90.9%	Pred. No. 6e-30		
Matches 50: Conservative	2	Mismatches	3	Indels 0
				Gaps 0

```
QY      1 CELYRMSTYSTFEAGVPVSESLRAGFYTTGVNDKVKCCFCGLMLDNNKKRGDSP 55  
        |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||  
Db     28 CELYRLSTYSAPPGVPVSERSLRAGFYTTGANDKVKPCCGLMLDNNKKRGDSP 82
```

RESULT 12
US-09-201-936-17
: Sequence 17. Application US/09201936

```

? APPLICANT: Korneiluk, Robert G.
? APPLICANT: McKenzle, Alexander E.
? APPLICANT: Balrd, Stephen
? APPLICANT: Liston, Peter
? TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
? TITLE OF INVENTION: PROBES, AND DETECTION METHODS
? FILE REFERENCE: 07891/003003
? CURRENT APPLICATION NUMBER: US/09/201,936
? CURRENT FILING DATE: 1998-12-01
? EARLIER APPLICATION NUMBER: 09/011,356
? EARLIER FILING DATE: 1998-02-04
? EARLIER APPLICATION NUMBER: PCT/IB96/01022
? EARLIER FILING DATE: 1996-08-05
? EARLIER APPLICATION NUMBER: 08/576,956
? EARLIER FILING DATE: 1995-12-22
? EARLIER APPLICATION NUMBER: 08/511,485
? EARLIER FILING DATE: 1995-08-04
? NUMBER OF SEQ ID NOS: 45
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO: 17
? LENGTH: 68
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-201-936-17

```

Query Match	51.3%	Score 158;	DB 9;	length 68;
Best Local Similarity	52.8%;	Pred. No. 7.6e-14;		
Matches 28; Conservative	8;	Mismatches 17;	Indels 0;	Gaps 0

Oy 2 ELYRMSTYSTEPAGVPVSEKSLARAGFYITGVNDKVKEFCGGLMDNWKRGDS 54
| | :
Db 1 EENRLKTFANFSGSPVASASTLARAGFLYTGEGDIVRCSCHAAVDNRWQYGDS 53

```

RESULT 13
US-09-965-967-22
; Sequence 22, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256,830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 110
; TYPE: prt
;

```


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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:58:42 ; Search time 6.01959 Seconds

(Without alignments)
878.365 Million cell updates/sec

Title: US-08-569-749-6

Perfect score: 308

Sequence: 1 CELYRMSTYTFPACVPVSE.....KVKCFCCGLMDNMRKRGDSP 55

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	308	100.0	604	2	S68449	apoptosis inhibitor
2	301	97.7	618	2	S68450	apoptosis inhibitor
3	158	51.3	497	2	S69544	apoptosis inhibitor
4	141	45.8	358	2	JC5964	apoptosis inhibitor
5	133	43.2	268	2	T10304	inhibitor of apopt
6	133	43.2	268	2	A53989	apoptosis-inhibiti
7	128	41.6	1232	2	A55478	neuronal apoptosis
8	126	40.9	208	2	T03183	probable apoptosis
9	125	40.6	1447	2	T42628	neuronal apoptosis
10	124	40.3	298	2	JC7568	kidney inhibitor o
11	106.5	34.6	275	2	A45679	inhibitor-of-apopt
12	106	34.4	496	2	S68452	apoptosis inhibitor
13	106	34.4	497	2	S69545	apoptosis inhibitor
14	102	33.1	150	2	T28409	ORF MSV248 probabl
15	94	30.5	275	2	T10310	apoptosis-inhibiti
16	83.5	27.1	286	2	D36828	Orf13 protein - Au
17	83.5	27.1	292	2	T41772	Orf13 protein - Au
18	77	25.0	155	2	T30489	apoptosis inhibitor
19	74.5	24.2	997	2	T43523	cutl17 protein - fi
20	72.5	23.5	234	2	T30427	probable apoptosis
21	72.5	23.5	4845	2	T31067	BIR repeat contain
22	65	21.1	329	2	T28403	ORF MSV242 probabl
23	60	19.5	932	2	H86325	hypothetical prote
24	59	19.2	733	2	T04070	hypothetical prote
25	58	18.8	288	2	B72272	thrombin (EC 3.4.2
26	57.5	18.7	236	2	C42696	hypothetical prote
27	57.5	18.7	337	2	T27615	ecarin precursor -
28	57.5	18.7	616	2	A55796	3-methyl-adenine D
29	57	18.5	187	2	B98183	

30	57	18.5	187	2	F86029	3-methyladenine DN
31	57	18.5	707	2	T40070	origin recognition
32	57	18.5	1401	2	T17452	Werner syndrome pr
33	57	18.5	1401	2	T30247	Werner syndrome pr
34	57	18.5	1930	2	F86200	protein F12K11.17
35	56.5	18.3	1192	2	G70513	5-methyltetrahydro
36	55.5	18.0	617	2	S10511	thrombin (EC 3.4.2
37	55.5	18.0	618	2	A35827	thrombin (EC 3.4.2
38	55	17.9	249	2	H72858	apoptosis inhibitor
39	55	17.9	422	2	G90259	hypothetical prote
40	55	17.9	422	2	H90271	hypothetical prote
41	55	17.9	422	2	H90275	hypothetical prote
42	55	17.9	422	2	H90501	hypothetical prote
43	55	17.9	422	2	B90327	hypothetical prote
44	55	17.9	1156	2	T14899	aminophospholipid
45	54.5	17.7	155	2	T37471	apoptosis inhibitor

ALIGNMENTS

RESULT 1

S68449

apoptosis inhibitor hlap-1 - human

C:Species: Homo sapiens (man)

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000

C:Accession: S68449

R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha

Nature 379, 349-353, 1996

A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of

A:Reference number: A58182; MUID:96149249; PMID:8552191

A:Accession: S68449

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-604 <LIS>

A:Cross-references: EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g1184316

C:Function:

A:Description: apoptotic suppressor

C:Superfamily: RING finger homology

C:Keywords: apoptosis; zinc finger

F:553-597/Domain: RING finger homology <RNG>

Query Match 100.0%; Score 308; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 2.4e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CELYRMSTYTFPACVPVSESLRAGFYTGVDKVCFCGCLMDNMRKRGDSP 55

DB 28 CELYRMSTYTFPACVPVSESLRAGFYTGVDKVCFCGCLMDNMRKRGDSP 82

RESULT 2

S68450

apoptosis inhibitor hlap-2 - human

C:Species: Homo sapiens (man)

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000

C:Accession: S68450

R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha

Nature 379, 349-353, 1996

A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of

A:Reference number: A58182; MUID:96149249; PMID:8552191

A:Accession: S68450

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-618 <LIS>

A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318

C:Function:

A:Description: apoptotic suppressor

C:Superfamily: RING finger homology

C:Keywords: apoptosis; zinc finger

Query Match 97.7%; Score 301; DB 2; Length 618;

A;Cross-references: GB:U19251
C;Genetics:
A;Gene: GDB:SMA@; SMA
A;Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A;Map position: 5q12.2-5q13
C;Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prot
F;94-110/Domain: transmembrane #status predicted <TM1>
F;470-477/Region: nucleotide-binding motif A (P-loop)
F;479-496/Domain: transmembrane #status predicted <TM2>
F;476/Binding site: ATP (Lys) #status predicted
F;618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.6%; Score 128; DB 2; Length 1232;
Best Local Similarity 40.7%; Pred. No. 4.6e-08;
Matches 22; Conservative 11; Mismatches 31; Indels 0; Gaps 0;

OY 2 ELYRMSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 55
DB 278 EELRLDSFRDMPRESAVGVALAKAGLFYTGITKIDIVQCFSCGGCLEKWKQEGDDP 331

RESULT 8
T03183
probable apoptosis inhibitor - Chilo iridescent virus
C;Species: Chilo iridescent virus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Sep-2000
C;Accession: T03183
R;Bahar, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A;Reference number: 214834; MUID:98141693; PMID:9482589
A;Accession: T03183
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-208 <BAH>
A;Cross-references: EMBL:AF003534; NID:g2738385; PIRN:AAB94481.1; PID:g2738454
C;Superfamily: RING finger homology
F;159-202/Domain: RING finger homology <RRN>

Query Match 40.9%; Score 126; DB 2; Length 208;
Best Local Similarity 41.2%; Pred. No. 1.6e-08;
Matches 21; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

OY 5 RMSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 55
DB 40 RLNSFQNPQLPLPSKEQLSRAGFIYINIGDOVQCFYCDLKEKWRSDNP 90

RESULT 9
T42628
neuronal apoptosis inhibitory protein 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T42628
R;Varaghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.
Mamm. Genome 10, 761-763, 1999
A;Title: CDNA cloning and the 5' genomic organization of Naip2, a candidate gene for mur
A;Reference number: Z22179; MUID:99315342; PMID:10384056
A;Accession: T42628
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1447 <YAR>
A;Cross-references: EMBL:AF102871; NID:g3860228; PID:g3860229; PIRN:AAC73002.1
C;Genetics:
A;Gene: Naip2

Query Match 40.6%; Score 125; DB 2; Length 1447;
Best Local Similarity 40.7%; Pred. No. 1.3e-07;
Matches 22; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

OY 2 ELYRMSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 55
DB 278 EELRLDSFRDMPRESAVGVALAKAGLFYTGITKIDIVQCFSCGGCLEKWKQEGDDP 331

RESULT 10
JC7568
kidney inhibitor of apoptosis protein - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7568
R;Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
Biochem. Biophys. Res. Commun. 279, 820-831, 2000
A;Title: KIAIP, a novel member of the inhibitor of apoptosis protein family.
A;Reference number: JC7568; MUID: 21092523; PMID:1162435
A;Accession: JC7568
A;Molecule type: mRNA
A;Residues: 1-298 <LIN>
C;Comment: This protein, a new member of the inhibitor of apoptosis protein family, p

C;Genetics:
A;Gene: Kiaip
A;Map position: 20q13.3
C;Keywords: apoptosis

Query Match 40.3%; Score 124; DB 2; Length 298;
Best Local Similarity 44.4%; Pred. No. 4.1e-08;
Matches 24; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

OY 2 ELYRMSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 55
DB 87 EELRLASFDWPLTAIEVPELLAAGFFHTGHODKVCFCFCYGGLOSKWRGDDP 140

RESULT 11
A45679
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C;Species: Cydia pomonella granulosis virus CpGV
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
C;Accession: A45679
R;Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A;Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A;Reference number: A45679; MUID:93188168; PMID:8445726
A;Accession: A45679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <CRO>
A;Cross-references: GB:I05494; NID:g289583; PIRN:AAA43835.1; PID:g289584
A;Note: sequence extracted from NCBI backbone (NCBIT:127014, NCBI:P:127015)
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 34.6%; Score 106.5; DB 2; Length 275;
Best Local Similarity 35.2%; Pred. No. 6.5e-06;
Matches 19; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

OY 2 ELYRMSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNWKRGDSP 55
DB 7 EEVRLNTEFKWPSF-LSPETMAKNGFYLLGRSDEVCAFCVKEIMRKKEGEDP 59

RESULT 12
S68452
apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Nov-2000
C;Accession: S68452; S78528
R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraba
Nature 379, 349-353, 1996
A;Title: Suppression of apoptosis in mammalian cells by Naip and a related family of
A;Reference number: A58182; MUID:96149249; PMID:8552191
A;Accession: S68452
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-496 <LIS>

A:Cross-references: EMBL:U45881; NID:g1184313; P1DN:AAC4698.1; PID:g1184314
R:Baïrd, S.D.
submitted to the EMBL Data Library, January 1996
A:Reference number: 578528
A:Accession: 578528
A:Molecule type: mRNA
A:Residues: 1-36, 'A', '37', 'K', '39', 'L', '41-44', 'H', '46-58', 'O', '60-412', 'A', '414-427', 'A', '429-496'
A:Cross-references: EMBL:U45881; NID:g1184313; P1DN:AAC4698.1; PID:g1184314
C:Genetics:
A:Cross-references: FlyBase:FBgn0015247
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homolog
C:Keywords: apoptosis; zinc finger
E:445-489/Domain: RING finger homolog <RING>

Query Match	34.4%;	Score 106;	DB 2;	Length 496;
Best Local Similarity	34.5%;	Pred. No. 1.3e+05;		
Matches 19; Conservative	13;	Mismatches 23;	Indels 0;	Gaps 0;

Oy 1 CEIYRMSTSYSTPPAGVPVSEKSLARAGFYTTGVNDKVCCIGMLDNKKRGDSP 55
 | :
Db 209 CVDARLRFTDWPISNIGPASALAQAGLYQKIGDVGFCHCNIGLRSQMKEDEP 263

RESULT 13
S69545

C:Species: *Drosophila melanogaster*
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S6495

R. Duckett, C.S.; Naya, V.E.; Gedrich, R.W.; Clem, R.J.; Van Dongen, J.L.; Giffillan, M.C.; EMBO J. 15, 2685-2694, 1996

A:Title: A conserved family of cellular genes related to the baculovirus iap gene and endoplasmic reticulum chaperones
A:Reference number: S69544; NUID:96256286; PMID:6654366
A:Accession: S69545

A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-497 <DUC>

A:Cross-references: EMBL:U32373; NID:g1019116; PIDN:ACA7155.1; PID:g1019117
C:Genetics:
A:Gene: 11p

C; Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
E; 446-490/Domain: RING finger homology <RRN>

Query Match	34.48;	Score 106;	DB 2;	Length 497;
Best Local Similarity	34.5%;	Pred. NO. 1.3e-05;		
Matches 19;	Conservative 13;	Mismatches 23;	Indels 0;	Gaps 0;

QY 1 CELIYKMTSYSTPPAGVSVSRSLARACGYTTGTGNDKKVKCFCCGIMLDNWKRGDSP 55
| : : : : | : : : : | : : : : | : : : : |
Db 211 CYDARLETFETDPISNTQPASALAQAAGLYQKIGDVYGFCHCNIGLRSMQKEDEP 265

RESULT 14
T28409

C:Species: Melanoplus sanguinipes entomopoxvirus
ORF MSV248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession T28409
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oama, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999

A/Title: The genome of *Melanoplus sanguinipes* entomopoxvirus
A/Reference number: Z20484; MUID:99102612; PMID:9847359
A/Accession: T28409

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-150 <AFO>

A:Cross-References: EMBL:AF063886; NITD:g40496647; PIDN:PAC97724.1; PID:g40497644
C:Genetics:
A:Note: MSV248

Query Match	33.1%;	Score 102;	DB 2;	Length 150;
-------------	--------	------------	-------	-------------

```
Best Local Similarity 35.38; Pred. No. 1.4e-05;
Matches 18; Conservative 9; Mismatches 24; Indels 0; Gaps 0;
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DQ 5 RMSTYTFPAGVYVSERSLARAGFYTTGVNDKVKFCGGLMDNWKRGDSP 55
|::: | : | ||| : | | | : | :
DQ 19 RINSLENWPISELFKINRLCEAGFPTNIGDITVCNGCGLIKKNMLYYNDP 69

RESULT 15
T10310

C:Species: *Oryzia pseudotsugata* nuclear polyhedrosis virus, OpNPV
C:Date: 16-Jul-1999 #sequence, rev1sion 16-Jul-1999 #text_change 15-Sep-2000
C:16-Jul-1999 #sequence, rev1sion 16-Jul-1999 #text_change 15-Sep-2000

C:Accession:TI10310
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virolology 229, 381-399, 1997

A>Title: The sequence of the *Oryzja pseudotsugata* multilnucleocapsid nuclear
 A:Reference number: Z17011, MUID:97271300, PMID:9126251
 A:Accession: T10310

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-275 <AHR>

A:Cross-references: EMBL:U75930; NID:G2934903; PIDN:AAC59040.1; PID:g1911288
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
E:223-268/Domain:RING finger homology <RNF>

Query Match	30.5%	Score	94	DB 2	Length	275
Best Local Similarity	31.4%	Pred.	No.	0.00026		

Matches	16;	Conservative	11;	Mismatches	24;	Indels	0;	Gaps	0.
5	RMSTSTTEPDAGVPSERSLARAGFYMTGVNDKRCFCGCGI.M.DNWKRDSP	55							

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129 RRATFDHWPALNALTHDIAEAGMFHTMLGDEFACFCDCRVRDWLPGGDP 179

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Search completed: May 5, 2003, 16:08:07
Job time : 7.01959 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 2.2811 Seconds

(Without alignments)
1000.040 Million cell updates/sec

Title: US-08-569-749-6

Sequence: 308 1 CELYRMSYTFEPAGVPVSE.....KVACFCGGLMDNMRKRDSP 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	308	100.0	604	1 BIR2_HUMAN	Q13489 homo sapien
2	301	97.7	618	1 BIR3_HUMAN	Q13490 homo sapien
3	294	95.5	612	1 BIR3_MOUSE	Q62210 mus musculu
4	287	93.2	600	1 BIR2_MOUSE	Q08863 mus musculu
5	248	80.5	611	1 BIR1_CHICK	Q90660 gallus galli
6	158	51.3	497	1 BIR4_HUMAN	P98170 homo sapien
7	152	49.4	496	1 BIR4_MOUSE	Q60989 mus musculu
8	151	49.0	496	1 BIR4_RAT	Q9R016 rattus norv
9	141	45.8	358	1 PIAP_PIG	Q62640 sus scrofa
10	137	44.5	1402	1 BIRG_MOUSE	Q9J1B3 sus musculu
11	137	44.5	1403	1 BIRE_MOUSE	Q9R016 mus musculu
12	136	44.2	1403	1 BIRF_MOUSE	Q9J1B6 mus musculu
13	133	43.2	268	1 IAP1_NPVOP	P41437 oryza pseu
14	129	41.9	438	1 IAP1_DROME	Q24306 drosophila
15	128	41.6	1403	1 BIR1_HUMAN	Q13075 homo sapien
16	126	40.9	239	1 ZFP_IRV6	P47732 chilo iride
17	125	40.6	1447	1 BIRB_MOUSE	Q9GUK4 mus musculu
18	124	40.3	298	1 BIR7_HUMAN	Q96CA5 homo sapien
19	112	36.4	236	1 BIR8_HUMAN	Q96P09 homo sapien
20	112	36.4	1403	1 BIRA_MOUSE	Q9GUK5 mus musculu
21	109	35.4	236	1 BIR8_PANTR	Q95M72 pan troglod
22	107	34.7	236	1 BIR8_GORGO	Q95M71 gorilla gor
23	106.5	34.6	275	1 IAP1_GVCP	P41436 cydia pomon
24	106	34.4	275	1 IAP2_DROME	Q24307 drosophila
25	94	30.5	275	1 IAP1_NPVOP	Q10296 oryza pseu
26	83.5	27.1	286	1 IAP1_NPVAC	P41435 autographa
27	75	24.4	224	1 IAPL_ASFB7	Q65138 african swi
28	74.5	24.2	142	1 BIR5_HUMAN	Q15392 homo sapien
29	74.5	24.2	997	1 BIR1_SCHPO	Q14064 schizosacch
30	72.5	23.5	4829	1 BIR6_HUMAN	Q9NR09 homo sapien
31	71.5	23.2	140	1 BIR5_MOUSE	Q70201 mus musculu
32	68.5	22.2	224	1 IAPL_ASFC3	Q11451 african swi
33	68.5	22.2	224	1 IAPL_ASFC4	Q12407 african swi

34	68.5	22.2	224	1 IAPL_ASFM1	Q11452 african swi
35	68.5	22.2	238	1 IAPL_ASFM2	Q11453 african swi
36	62.5	20.3	142	1 BIR5_RAT	Q9J1H7 rattus norv
37	57	18.5	707	1 ORC1_SCHPO	P54789 schizosacch
38	57	18.5	1401	1 WRN_MOUSE	C09053 mus musculu
39	56.5	18.3	1192	1 METH_MYCTU	O33255 mycobacteri
40	55.5	18.0	617	1 THRB_MOUSE	P18292 rattus norv
41	55.5	18.0	618	1 THRB_RAT	P19221 mus musculu
42	55	17.9	249	1 IAP2_NPVAC	P41454 autographa
43	54.5	17.7	244	1 Y2BK_SSV1	P20213 sulfobus
44	54	17.5	203	1 CHPE_PSEAE	Q87005 pseudomonas
45	54	17.5	958	1 YBS3_YEAST	P38086 saccharomyc

ALIGNMENTS

RESULT 1
BIR2_HUMAN STANDARD: PRT: 604 AA.
AC Q13489; Q16628; Q9UP46; Q9HC27;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (Inhibitor of apoptosis protein 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF signaling complex protein 1) (IAP homolog C).
DE BIR2 OR API1 OR IAP1 OR MIRC.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RP MEDLINE FROM N.A.
RX MEDLINE-96128127; PubMed-8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE-96149249; PubMed-8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.S.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";
RL Nature 379:349-353(1996).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE-96209843; PubMed-8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE-99252096; PubMed-10233894;
RA Horrevorts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J., ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis factor-alpha in vitro are expressed in atherosclerotic lesions, including inhibitor of apoptosis protein-1, stannin, and two novel genes.";
RL Blood 93:3418-3431(1999).
[5]
RP SEQUENCE OF 362-441 FROM N.A.
RX MEDLINE-20519161; PubMed-11066071;
RA Baens M., Steyis A., Dierlam J., De Wolf-Peters C., Marynen P.;
RT "Structure of the MIF gene and molecular characterization of the genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone

RT B-cell lymphomas of MALT type.";
RL Genes Chromosomes Cancer 29:281-291(2000).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC tissue). This translocation is found in approximately 50% of
CC cytogenetically abnormal low-grade MALT lymphoma and involves
CC MALTI and BIRC2.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL; L49432; AAC41943.1; -;
DR EMBL; U45878; AAC50371.1; -;
DR EMBL; U37546; AAC50507.1; -;
DR EMBL; AF070674; AAC83232.1; -;
DR EMBL; AF178945; AAG09369.1; -;
DR HSSP; Q13490; IOBH.
DR Genew; HGNC:591; BIRC3.
DR MIM; 601712; -;
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; ZnF_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Apoptosis; zinc-finger; Repeat; Chromosomal translocation.
FT REPEAT 29 96 BIR 1.
FT REPEAT 169 235 BIR 2.
FT REPEAT 255 322 BIR 3.
FT DOMAIN 439 529 CARD.
FT ZN_FING 557 592 RING-TYPE.
FT SITE 442 443 BREAKPOINT FOR TRANSLOCATION TO FORM
FT BIRC2-MALTI1.
FT CONFLICT 18 18 N -> Y (IN REF. 4).
FT CONFLICT 119 119 N -> H (IN REF. 2).
FT CONFLICT 153 153 D -> E (IN REF. 2).
FT CONFLICT 163 163 H -> P (IN REF. 2).
FT CONFLICT 165 165 A -> R (IN REF. 2).
FT CONFLICT 191 191 K -> R (IN REF. 2).
FT CONFLICT 191 191 F -> L (IN REF. 2).
FT CONFLICT 364 364 Q -> P (IN REF. 2).
SQ SEQUENCE 604 AA; 68371 MW; 8581A00BA9AAB4A7 CRC64;
Query Match 100.0%; Score 308; DB 1; Length 604;
Best Local Similarity 100.0%; Pred. No. 6.4e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CELYRMSTYSPFAGVPSERSRLAGFYTGVDKVCFCGCLMDLMDNRGDS 55
DB 28 CELYRMSTYSPFAGVPSERSRLAGFYTGVDKVCFCGCLMDLMDNRGDS 82
RESULT 2
BIR3_HUMAN
ID BIR3_HUMAN STANDARD; PRT; 618 AA.
AC Q13490; Q16516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
DE protein 2) (HIAF2) (HIAF-2) (C-IAP1) (TNFR2-TRAF signaling complex
DE protein 2) (IAP homolog B).
GN BIRC3 OR API2 OR IAP2 OR MIH3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96128127; PubMed-8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-96149249; PubMed-8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-96209843; PubMed-8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-99332054; PubMed-10404221;
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)
RT repeat.";
RL Nat. Struct. Biol. 6:648-651(1999).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

```
CC -! DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobloggen.fr/services/chromocancer/Genes/BIRC1D239.html".
CC -----
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CC -----
DR EMBL: L49431; AAC41942.1; -
DR EMBL: U45879; AAC50372.1; -
DR EMBL: U37547; AAC50508.1; -
DR EMBL: BC016174; AAH16174.1; -
DR PDB: 1QBH; 20-OCT-99.
DR Genew: HGNC:590; BIRC2.
DR MIM: 601721; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis: Zinc-finger; Repeat; 3d-structure.
DR REPEAT 46 113 BIR 1.
DR REPEAT 184 250 BIR 2.
DR REPEAT 269 336 BIR 3.
DR DOMAIN 453 543 CARD.
DR ZN_FING 571 606 RING-TYPE.
DR CONFLICT 157 157 S -> P (IN REF. 2).
DR CONFLICT 308 308 C -> G (IN REF. 2).
DR CONFLICT 414 414 Q -> L (IN REF. 2).
DR CONFLICT 514 514 L -> W (IN REF. 2).
DR CONFLICT 514 514 L -> W (IN REF. 2).
DR SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 97.7%; Score 301; DB 1; Length 618;
Best Local Similarity 98.2%; Pred. No. 5.5e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 55
Db 45 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 99

RESULT 3
BIR3_MOUSE STANDARD; PRT; 612 AA.
AC Q62210; O08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral iAP repeat-containing protein 3 (Inhibitor of apoptosis
DE protein 2) (MIAP2) (MIAP-2).
GN BIRC3 OR API2 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
```

```
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes".
RL Genomics 46:495-503(1997).
CC -! FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -! SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -! TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -! SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -! SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -! SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -! SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: L49433; AAC42078.1; -
DR EMBL: U88909; AAC53532.1; -
DR HSSP: Q13490; 1QBH.
DR MGD: MGI:1197009; Birc3.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis: Zinc-finger; Repeat.
DR REPEAT 46 113 BIR 1.
DR REPEAT 177 243 BIR 2.
DR REPEAT 262 329 BIR 3.
DR DOMAIN 447 537 CARD.
DR ZN_FING 565 600 RING-TYPE.
DR CONFLICT 380 380 E -> K (IN REF. 2).
DR SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 95.5%; Score 294; DB 1; Length 612;
Best Local Similarity 94.5%; Pred. No. 4.6e-31;
Matches 52; Conservative 1; Mismatches* 2; Indels 0; Gaps 0;

QY 1 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 55
Db 45 CELYRMSTYTFPAGVPVSESLARAGFYTTGVNDKVCFCGGLMDNMKRGDSP 99

RESULT 4
BIR2_MOUSE STANDARD; PRT; 600 AA.
AC Q08863;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
```

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 1) (MIAPI) (MAP-1).
GN BIRC2 OR Apil OR IAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Loston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH SMAC AND WITH PRSS25; THESE INTERACTIONS
CC INHIBIT APOPTOTIC SUPPRESSOR ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (Potential).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U88908; AAC53531.1; -.
DR HSSP: Q13490; IOBH.
DR MCD: MGI:1197007; Birc2.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat.
KW REPEAT 27 94 BIR 1.
FT REPEAT 167 233 BIR 2.
FT REPEAT 253 320 BIR 3.
FT DOMAIN 436 525 CARD.
FT ZN_FING 553 588 RING-TYPE.
SQ SEQUENCE 600 AA; 67198 MW; AD7F73E6849317D1 CRC64;

Query Match 93.2%; Score 287; DB 1; Length 600;
Best Local Similarity 90.9%; Pred. No. 3.8e-30;
Matches 50; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVCFCGCIIMLDNMKRGDSP 55
DB 26 CELYRLSTYSAFPGRVPSERSLARAGFYTGANDKVCFCGCIIMLDNMKQGDSP 80

RESULT 5
BIR_CHICK
ID BIR_CHICK STANDARD; PRT; 611 AA.

AC Q90660;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis
DE protein).
GN IYA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=9710112; PubMed=8945639;
RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT "IYA, a vertebrate homologue of IAP that is expressed in T
RT lymphocytes."
RL DNA Cell Biol. 15:981-988(1996).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U27466; AAB48118.1; -.
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat; Nuclear protein.
KW REPEAT 30 97 BIR 1.
FT REPEAT 176 242 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 446 536 CARD.
FT ZN_FING 564 599 RING-TYPE.
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;

Query Match 80.5%; Score 248; DB 1; Length 611;
Best Local Similarity 81.5%; Pred. No. 5.3e-25;
Matches 44; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 CELYRMSTYSTFPAGVPVSESLARAGFYTGVDKVCFCGCIIMLDNMKRGDS 54
DB 29 CELYRMSTSTFPVNVPSERSLARAGFYTGVDKVCFCGCLVLDNMQPDN 82

RESULT 6

BIR4_HUMAN	STANDARD:	PRT:	497 AA.
AC	P98170; Q9NQ14;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)		
DE	(IAP-like protein) (HILP).		
GN	BIRC4 OR API3 OR IAP3 OR XIAP.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Fetal brain;		
RX	MEDLINE-96149249; PubMed-8552191;		
RA	Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertton-Horvat G.		
RA	Farahani R., Mclean M., Ikeda J., Mackenzie A., Korneluk R.G.;		
RT	"Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes."		
RL	Nature 379:349-353(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Fetal heart;		
RX	MEDLINE-96256286; PubMed-8654366;		
RA	Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,		
RA	Gillfillan M.C., Shields H., Hardwick J.M., Thompson C.B.;		
RT	"A conserved family of cellular genes related to the baculovirus IAP gene and encoding apoptosis inhibitors."		
RL	EMBO J. 15:2685-2694(1996).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Grafham D.;		
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	FUNCTION.		
RX	MEDLINE-97373959; PubMed-9230442;		
RA	Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;		
RT	"X-linked IAP is a direct inhibitor of cell-death proteases."		
RL	Nature 388:300-304(1997).		
RN	[5]		
RP	MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.		
RX	MEDLINE-21634829; PubMed-11604410;		
RA	Verhagen A.M., Slike J., Ekert P.G., Pakusch M., Kaufmann H.,		
RA	Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L.,		
RA	Simpson R.J., Vaux D.L.;		
RT	"HRA2 promotes cell death through its serine protease activity and its ability to antagonize inhibitor of apoptosis proteins."		
RL	J. Biol. Chem. 277:445-454(2002).		
RN	[6]		
RP	STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.		
RX	MEDLINE-21020961; PubMed-11140637;		
RA	Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.,		
RA	Herrman J., Wu J.C., Fesik S.W.;		
RT	"Structural basis for binding of Smac/DIABLO to the XIAP BIR3 domain."		
RL	Nature 408:1004-1008(2000).		
CC	-1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9		
CC	-1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions		
CC	inhibit apoptotic suppressor activity.		
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.		
CC	-1- TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD		
CC	LEUKOCYTES.		
CC	-1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3		
CC	and -7, while the third BIR is involved in caspase-9 inhibition.		
CC	The interactions with SMAC and PRSS25 are mediated by the second		
CC	and third BIR domains.		
CC	-1- SIMILARITY: BELONGS TO THE IAP FAMILY.		
CC	-1- SIMILARITY: CONTAINS 3 BIR REPEATS.		
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		
CC	-----		

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CC      -----
DR      EMBL; U45880; AAC50373.1; -.
DR      EMBL; U32974; AAC50518.1; -.
DR      EMBL; AL121601; CAB95312.1; -.
DR      PDB; 1G3F; 10-JAN-01.
DR      Genew; HGNC:592; BIRC4.
DR      MIM; 300079; -.
DR      InterPro; IPR001370; BIR.
DR      InterPro; IPR001841; znf_rlng.
DR      Pfam; PF00097; zf-C3HC4; 1.
DR      Pfam; PF00653; BIR; 3.
DR      SMART; SM00238; BIR; 3.
DR      SMART; SM00184; RING; 1.
-DR      PROSITE; PS01282; BIR_REPEAT_1; 3.
DR      PROSITE; PS50143; BIR_REPEAT_2; 3.
DR      PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR      PROSITE; PS50089; ZF_RING_2; 1.
DR      Apoptosis; zinc-finger; Repeat; Thiol protease inhibitor;
KW      3d-structure.
KM      REPEAT      26      93      BIR 1.
FT      REPEAT      163      230      BIR 2.
FT      REPEAT      265      330      BIR 3.
FT      ZN_FING      450      485      RING-TYPE.
FT      MUTAGEN      214      214      D->S: REDUCED INTERACTION WITH PRSS25.
FT      MUTAGEN      314      314      E->S: DECREASED INTERACTION WITH SMAC AND
FT      CONFLICT      162      162      S -> C (IN REF. 1).
FT      CONFLICT      423      423      Q -> P (IN REF. 2).
SO      SEQUENCE      497 AA; 56684 MW; 9D394C16D45EB635 CRC64;

Query Match
Best Local Similarity 51.3%; Score 158; DB 1; Length 497;
Matches 28; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY      2 ELYRMSTYSTPPAGVPYSESLARAGFYTYGNDKVCFCGCGILMDMWRGDS 54
DB      26 EENRLKTFANFPSSGPVSASTLARAGFLYTGEQDVTVCFSCHAAVDHWQYDGS 78

RESULT 7
BIR4_MOUSE
ID      BIR4_MOUSE      STANDARD;      PRT;      496 AA.
AC      Q60989; 008865;
DT      01-NOV-1997 (Rel. 35, Created)
DT      15-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE      protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE      (IAP homolog A) (MIAP3) (MIAP-3).
GN      BIRC4 OR API3 OR XIAP OR AIP4 OR MIHA.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RX      [1]
RX      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX      MEDLINE=96209843; PubMed=8643514;
RA      Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RA      "Cloning and expression of apoptosis inhibitory protein homologs that
RT      function to inhibit apoptosis and/or bind tumor necrosis factor
RT      receptor-associated factors."
RL      Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN      [2]
RN      SEQUENCE FROM N.A.
RA      Farahani R., Lefebvre C., Korneljuk R.G., Mackenzie A.E.;

```

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U36842; AAC52594.1; -
CC EMBL: U88990; AAB58376.1; -
CC HSSP: Q13490; IQBH.
CC MGD: MGI:107572; Birc4.
CC InterPro: IPR001370; BIR.
CC InterPro: IPR001841; Znf_ring.
CC Pfam: PF00097; zf-C3HC4; 1.
CC SMART: SM00238; BIR; 3.
CC SMART: SM00184; RING; 1.
CC PROSITE: PS01282; BIR_REPEAT_1; 3.
CC PROSITE: PS0143; BIR_REPEAT_2; 3.
CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE: PS50089; ZF_RING_2; 1.
CC Apoptosis; Zinc-finger; Repeat.
CC REPEAT 26 93 BIR 1.
CC REPEAT 163 230 BIR 2.
CC REPEAT 264 329 BIR 3.
CC ZN_FING 449 484 RING-TYPE.
CC CONFLICT 208 208 E -> K (IN REF. 2).
CC CONFLICT 317 317 W -> D (IN REF. 2).
CC CONFLICT 322 322 S -> C (IN REF. 2).
CC CONFLICT 346 346 S -> P (IN REF. 2).
CC CONFLICT 360 360 I -> L (IN REF. 2).
CC CONFLICT 388 388 C -> S (IN REF. 2).
CC CONFLICT 449 449 V -> F (IN REF. 2).
CC CONFLICT 462 462 V -> A (IN REF. 2).
CC CONFLICT 468 468 K -> N (IN REF. 2).
CC CONFLICT 490 490
CC SEQUENCE 496 AA; 56079 MW; ECSFAE0799F2CDDH CRC64;
Query Match 49.4%; Score 152; DB 1; Length 496;
Best Local Similarity 50.9%; Pred. No. 2e-12;
Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
OY 2 ELYRMSTYTFPAGVPVSERSLARAGFYTGVDKVKCCGGLMDNKKRGDS 54
DB 26 EFNRLKTFANFPSSPVASSTLARAGFLYTGEGDTVQCFSCHAAIDRWQYDGS 78
RESULT 8
BIR4_RAT
ID BIR4_RAT STANDARD; PRT; 496 AA.
AC Q9R016;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (RIAP3) (RIAP-3).
DE BIRC4 OR API3 OR XIAP.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Saito N.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AB033366; BAAB5304.1; -
CC HSSP: Q13490; IQBH.
CC InterPro: IPR001370; BIR.
CC InterPro: IPR001841; Znf_ring.
CC Pfam: PF00097; zf-C3HC4; 1.
CC Pfam: PF00653; BIR; 3.
CC SMART: SM00238; BIR; 3.
CC SMART: SM00184; RING; 1.
CC PROSITE: PS01282; BIR_REPEAT_1; 3.
CC PROSITE: PS0143; BIR_REPEAT_2; 3.
CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE: PS50089; ZF_RING_2; 1.
CC Apoptosis; Zinc-finger; Repeat.
CC REPEAT 26 93 BIR 1.
CC REPEAT 163 230 BIR 2.
CC REPEAT 264 329 BIR 3.
CC ZN_FING 449 484 RING-TYPE.
CC SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;
Query Match 49.0%; Score 151; DB 1; Length 496;
Best Local Similarity 50.9%; Pred. No. 2.7e-12;
Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
OY 2 ELYRMSTYTFPAGVPVSERSLARAGFYTGVDKVKCCGGLMDNKKRGDS 54
DB 26 EFNRLKTFANFPSSPVASSTLARAGFLYTGEGDTVQCFSCHAAVDRWQYDGS 78
RESULT 9
PIAP_PIG
ID PIAP_PIG STANDARD; PRT; 358 AA.
AC O62640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative inhibitor of apoptosis.
DE PIAP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.

RT atrophy candidate genes SMN and NAIP.";
 RL Genomics 48:121-127(1998).
 RN [3]
 RP SEQUENCE OF 386-623 FROM N.A.
 RA der Steege G., Draaijers T.G., Grootscholten P.M., Ozinga J.,
 RA Anzevino R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,
 RA Buys C.H.C.M.;
 RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 222-1403 FROM N.A.
 RA Jones K., Graves T., McPherson J.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP FUNCTION.
 RC TISSUE=Liver;
 RX MEDLINE=96149249; PubMed=8552191;
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
 RA Farhah R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related
 RT family of IAP genes.";
 RL Nature 379:349-353(1996).
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 CC SIGNALS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY
 CC NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN
 CC SPINAL CORD.
 CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN
 CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY (TYPE I (SMA TYPE 1), SMAS
 CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE 1
 CC (WERDNIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE
 CC III (WOLFFHART-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF
 CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE
 CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO
 CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
 CC NEWBORNS.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC -----
 DR EMBL; U19251; AAC52045.1; -;
 DR EMBL; U80017; AAC52047.1; -;
 DR EMBL; U21913; AAA64504.1; -;
 DR EMBL; AC005031; AAC62261.1; -;
 DR HSSP; Q13490; IOBH.
 DR Genew; HGNC:7634; BIRCL.
 DR MIM; 600355; -;
 DR InterPro: IPR001370; BIR.
 DR Pfam; PF00653; BIR; 3.
 DR SMART; SM00238; BIR; 3.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50837; NACHT; 1.
 KW Apoptosis; Repeat.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.
 FT REPEAT 278 345 BIR 3.
 FT DOMAIN 464 758 NACHT.
 FT CONFLICT 222 223 PK -> YR (IN REF. 4).
 FT CONFLICT 386 387 VP -> ST (IN REF. 3).
 FT CONFLICT 535 535 M -> V (IN REF. 3).
 FT CONFLICT 553 553 Y -> H (IN REF. 3).
 FT CONFLICT 1228 1231 MISSING (IN REF. 4).
 SQ SEQUENCE 1403 AA; 159613 MW; 566304C154DA5E64 CRC64;

Query Match 41.6%; Score 128; DB 1; Length 1403;
 Best Local Similarity 40.7%; Pred. No. 8.3e-09;

Matches 22; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 2 ELYRMSYVSTPPAGVVSERSLARGFYTYGVNDKVKCCGMLDNNKRGDSP 55
 Db 278 EELRLDSFKDWPRESAVGVALAKAGLFYTGIKDIYQCFSCGGLKQEGDDP 331

Search completed: May 5, 2003, 16:02:44
 Job time : 4.28111 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:57:12 ; Search time 13.4332 Seconds

(without alignments)
843.627 Million cell updates/sec

Title: US-08-569-749-6

Perfect score: 308

Sequence: 1 CELYRMSTSTFPAGVPVSE.....KVKCFCCGLMDNMKRGDSP 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	301	97.7	602	11	Q9ESE9	Q9ESE9 rattus norv
2	294	95.5	589	11	Q9ESE8	Q9ESE8 rattus norv
3	294	95.5	589	11	Q9QZC6	Q9QZC6 rattus norv
4	284	92.2	374	11	Q921N0	Q921N0 mus musculu
5	248	80.5	324	13	Q9DDN2	Q9DDN2 gallus gall
6	248	80.5	610	13	Q57319	Q57319 gallus gall
7	192	62.3	628	13	Q8UWD2	Q8UWD2 brachydantio
8	158	51.3	405	13	Q8UWH2	Q8UWH2 brachydantio
9	158	51.3	493	13	Q8UVF8	Q8UVF8 gallus gall
10	151	49.0	496	11	Q9ESF0	Q9ESF0 rattus norv
11	151	49.0	501	11	Q9EQ05	Q9EQ05 rattus norv
12	151	49.0	501	11	Q9EQ04	Q9EQ04 rattus norv
13	145	47.1	264	12	Q9EN27	Q9EN27 amsacta moo
14	144	46.8	195	13	Q9IA70	Q9IA70 gallus gall
15	144	46.8	197	13	Q9IA69	Q9IA69 gallus gall
16	143	46.4	281	12	Q9YNL8	Q9YNL8 choristoneu

17	140	45.5	276	12	Q8QL95	Q8QL95 manestra co
18	139	45.1	517	11	Q8R4U8	Q8R4U8 rattus norv
19	137	44.5	597	11	Q9R015	Q9R015 mus musculu
20	132	42.9	224	11	Q8B642	Q8B642 rattus norv
21	129	41.9	438	5	Q9VUX5	Q9VUX5 drosophila
22	128	41.6	1160	4	Q8TDZ4	Q8TDZ4 homo sapien
23	127	41.2	208	12	Q91EW1	Q91EW1 cydia pomon
24	126	40.9	208	12	Q55770	Q55770 chilo iride
25	124	40.3	280	4	Q9HAP7	Q9HAP7 homo sapien
26	124	40.3	298	4	Q9H2A8	Q9H2A8 homo sapien
27	124	40.3	298	4	Q9GCA5	Q9GCA5 homo sapien
28	122	39.6	403	5	Q8WRD9	Q8WRD9 ochlerotatu
29	116	37.7	346	5	Q968T8	Q968T8 bombyx mori
30	115	37.3	402	5	Q8TE21	Q8TE21 aedes albop
31	114.5	37.2	153	5	Q9VEM2	Q9VEM2 drosophila
32	114	37.0	313	12	Q9J827	Q9J827 spodoptera
33	112	36.4	236	4	Q96RW5	Q96RW5 homo sapien
34	112	36.4	236	4	Q96P09	Q96P09 homo sapien
35	110	35.7	379	5	Q9U492	Q9U492 trichoplusi
36	109	35.4	236	6	Q95M72	Q95M72 pan troglod
37	109	35.4	377	5	Q9N707	Q9N707 spodoptera
38	108.5	35.2	276	12	Q89744	Q89744 buzura supp
39	107	34.7	106	4	Q96RW6	Q96RW6 homo sapien
40	107	34.7	236	6	Q95M71	Q95M71 gorilla gor
41	106	34.4	261	12	Q9QES9	Q9QES9 epiphyas po
42	106	34.4	498	5	Q96U03	Q96U03 drosophila
43	104	33.8	109	6	Q8MYV4	Q8MYV4 bos taurus
44	102	33.1	150	12	Q91VJ4	Q91VJ4 melanoplus
45	99.5	32.3	268	12	Q91F18	Q91F18 helicoverpa

ALIGNMENTS

RESULT 1
ID Q9ESE9 PRELIMINARY; PRT; 602 AA.
AC Q9ESE9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF183430; AAG22970.1; -.
DR HSSP; O13490; IOBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 602 AA; 67326 MW; CC91385EEA62DE5A CRC64;
Query Match 97.7%; Score 301; DB 11; Length 602;
Best Local Similarity 96.4%; Pred. No. 8.4e-32;
Matches 53; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RT "The apoptosis inhibitor ch-IAP1 is a direct transcriptional target of
RT v-Rel and c-Rel."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF311289; AAG42316.1; -.
DR HSSP; Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR NON_TER 324 324
SQ SEQUENCE 324 AA; 36567 MW; 5E2B89DEAE3733F3 CRC64;

Query Match 80.5%; Score 248; DB 13; Length 324;
Best Local Similarity 81.5%; Pred. No. 5.3e-25;
Matches 44; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 1 CELYRSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKRGDS 54
29 CELYRSTSTFPVNVPSERRLARAGFYTGVDKVCFCGGLVDMWQPGDN 82

RESULT 6
ID 057319 PRELIMINARY; PRT; 610 AA.
AC 057319;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Inhibitor of apoptosis protein 1 (IAP) (Inhibitor of T cell apoptosis
DE PROTEIN).
GN IAP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_Taxid-9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE-EMBRYONIC FIBROBLAST;
RX MEDLINE-98038801; PubMed-9372964;
RA You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a
RT mediator of the antiapoptotic activity of the v-Rel oncoprotein,"
RL Mol. Cell. Biol. 17:7328-7341(1997).
CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CC CELLS.
CC -1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF
CC THE V-REL-TRANSFORMED CELLS.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE
CC SPLEEN, THYMUS, BURSAS, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS
CC IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC -1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC PROCESS.
CC -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC -1- SIMILARITY: MEMBER OF THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF
CC APOPTOSIS PROTEIN REPEAT).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; AF008592; AAB88044.1; -.
DR HSSP; Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.

KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 30 97 BIR_REPEAT 1.
FT REPEAT 176 242 BIR_REPEAT 2.
FT REPEAT 262 329 BIR_REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; AD647619650844A6 CRC64;

Query Match 80.5%; Score 248; DB 13; Length 610;
Best Local Similarity 81.5%; Pred. No. 1.1e-24;
Matches 44; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 1 CELYRSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKRGDS 54
29 CELYRSTSTFPVNVPSERRLARAGFYTGVDKVCFCGGLVDMWQPGDN 82

RESULT 7
ID 080WD2 PRELIMINARY; PRT; 628 AA.
AC 080WD2;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Iap1.
GN IAP1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid-7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20373792; PubMed-10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442500; AAL33679.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; zf_RING_2; 1.
SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 62.3%; Score 192; DB 13; Length 628;
Best Local Similarity 61.1%; Pred. No. 3.7e-17;
Matches 33; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Db 2 ELYRSTSTFPAGVPVSESLARAGFYTGVDKVCFCGGLMDNWKRGDS 55
29 ELFRISTYAKFPTTAVERSLARAGFYTGVDKVCFCGGLVDMWQSGDCP 82

RESULT 8
ID 080WH2 PRELIMINARY; PRT; 405 AA.
AC 080WH2;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE XIAP.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20373792; PubMed-10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DE EMBL; AF439767; AAL32047.1; -
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; zf_RING_2; 1.
SQ SEQUENCE 405 AA; 45564 MW; A366E342D83BECAB CRC64;

Query Match 51.3%; Score 158; DB 13; Length 405;
Best Local Similarity 51.0%; Pred. No. 8.1e-13;
Matches 26; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 5 RMSTSTPAGVPVRSERSLARAGFYTGVDKVCFCGGLMDNKKRGDS 55
ID 140 RUSTFNMWPAFSPVREDLAEAGMYIGIDNVQCFCCGGSLSEWEGGDP 190
AC 08UVF8; PRELIMINARY; PRT; 493 AA.
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP
(IAP3)."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DE EMBL; AF451854; AAL47170.1; -
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; zf_RING_2; 1.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match 51.3%; Score 158; DB 13; Length 493;
Best Local Similarity 54.7%; Pred. No. 1e-12;
Matches 29; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 2 ELYRMSTSTPAGVPVRSERSLARAGFYTGVDKVCFCGGLMDNKKRGDS 54
ID 26 EHYRLGTVEEPHDCPVASALARAGFYTGEGDKVKCSCHTVEGWEPGDS 78
AC 09ESF0; PRELIMINARY; PRT; 496 AA.
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DE EMBL; AF183429; AAG22969.1; -
DR HSSP; Q13490; IQBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
KW Zinc-finger.
SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;

Query Match 49.0%; Score 151; DB 11; Length 496;
Best Local Similarity 50.9%; Pred. No. 8.9e-12;
Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 2 ELYRMSTSTPAGVPVRSERSLARAGFYTGVDKVCFCGGLMDNKKRGDS 54
ID 26 EENRLTFANPPSSPVASASTLARAGFLYTGEGDTVCSCSHAVDRNQYGDG 78
AC 09EQ05; PRELIMINARY; PRT; 501 AA.
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-WISTAR; TISSUE-OVARY;
RA Lareu R.R., Bradley C.K., Iacher M., Ellis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DE EMBL; AF304333; AAG41192.1; -
DR HSSP; Q13490; IQBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.

ID 091A69 PRELIMINARY; PRT; 197 AA.
AC 091A69;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRED FAYOUMI; TISSUE=SPLEEN;
RX MEDLINE=21158006; PubMed=11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
specific genes";
RL Poul. Sci. 80:284-288(2001).
DR EMBL; AF221083; AAF35320.1; -.
DR HSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match 46.8%; Score 144; DB 13; Length 197;
Best Local Similarity 51.0%; Pred. No. 2.7e-11;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 5 RMSTYSTFPAGVPSERSLARAGFYTGVDKVCFCGGLMDNWKRGDSP 55
DB 120 RVKTFINWPTRIYPVQPEQLADAGFYVGRNDVCKCFCGGLRCWESGDDP 170

Search completed: May 5, 2003, 16:06:25
Job time : 14.4332 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:50:57 ; Search time 10.8353 Seconds

(without alignments)
676.383 Million cell updates/sec

Title: US-08-569-749-6

Sequence: 1 CELXRMSYSTFPAGVPVSE.....KVKCFCCGLMDNMRKRDSP 55

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	308	100.0	55	18	AAW13548	Human c-IAP2 repea
2	308	100.0	604	18	AAW19747	Human inhibitor of
3	308	100.0	604	18	AAW19582	Human apoptosis in
4	308	100.0	604	18	AAW13546	Human c-IAP2. Hom
5	308	100.0	604	19	AAW69295	Human H1AP-1 prote
6	308	100.0	604	20	AAV52703	Human cellular inh
7	308	100.0	604	20	AAV33997	Human cellular inh
8	308	100.0	604	23	ABG5664	Human inhibitor of
9	308	100.0	1140	23	AAU97837	Human cysteine pro
10	308	100.0	1141	22	AB50694	Human APT2-MLT chl

11	301	97.7	55	18	AAW13547	Human c-IAP1 repea
12	301	97.7	306	22	AAU02925	Angiotensin conver
13	301	97.7	618	18	AAW19746	Human inhibitor of
14	301	97.7	618	18	AAW19583	Human apoptosis in
15	301	97.7	618	18	AAW13545	Human c-IAP1. Hom
16	301	97.7	618	19	AAW69296	Human H1AP-2 prote
17	301	97.7	618	20	AAV33998	Human cellular inh
18	301	97.7	618	23	ABG5665	Human inhibitor of
19	294	95.5	591	18	AAW19586	Mouse apoptosis in
20	294	95.5	591	23	ABG5668	Mouse inhibitor of
21	294	95.5	612	18	AAW13555	Mouse c-IAP. Mus
22	294	95.5	612	19	AAW69289	Murine H1AP-2 prot
23	287	93.2	600	19	AAW69298	Murine H1AP-1 prot
24	287	93.2	602	18	AAW19585	Mouse apoptosis in
25	287	93.2	602	23	ABG5667	Mouse inhibitor of
26	158	51.3	497	19	AAW19581	Human apoptosis in
27	158	51.3	497	18	AAW19584	Human XIAP protein
28	158	51.3	497	21	AAV99985	Human X-linked inh
29	158	51.3	497	21	AAV59451	Human XIAP protein
30	158	51.3	497	23	ABG5663	Human inhibitor of
31	152	49.4	496	18	AAW19745	Mouse inhibitor of
32	152	49.4	496	18	AAW19584	Mouse apoptosis in
33	152	49.4	496	19	AAW69297	Murine XIAP protei
34	152	49.4	496	23	ABG5666	Mouse inhibitor of
35	151	49.0	438	17	AAW04583	Human inhibitor of
36	146	47.4	464	23	AAU75747	Human inhibitor of
37	131	42.5	438	22	AB48191	Drosophila mutant
38	130.5	42.4	263	23	ABB09488	AMEPV baculovirus-
39	129	41.9	434	22	AB48195	Drosophila mutant
40	129	41.9	438	22	ABB61858	Drosophila melanog
41	129	41.9	438	22	ABB67347	Drosophila melanog
42	129	41.9	438	22	AB48188	Drosophila wild-ty
43	129	41.9	438	22	AB48189	Drosophila mutant
44	129	41.9	438	22	AB48190	Drosophila mutant
45	129	41.9	438	22	AB48192	Drosophila mutant

ALIGNMENTS

RESULT 1	AAW13548	standard; Protein; 55 AA.
ID	AAW13548	
XX	AAW13548;	
AC	22-JUL-1997	(first entry)
DT	XX	
DE	XX	Human c-IAP2 repeat 1.
XX	XX	
KW	XX	IAP; inhibitor; apoptosis; RING finger domain; restinosis;
XX	XX	myocardial infarction; nephritis; HIV.
OS	XX	Hom sapiens.
XX	XX	
PN	XX	W09706182-A1.
XX	XX	
PD	XX	20-FEB-1997.
XX	XX	
PF	XX	06-AUG-1996; 96WO-0512860.
XX	XX	
PR	XX	08-DEC-1995; 95US-0569749.
XX	XX	
PR	XX	08-AUG-1995; 95US-0512946.
XX	XX	
PA	XX	(TULIA-) TULARIK INC.
XX	XX	
PI	XX	Goeddel DV, Rothe M.
XX	XX	
DR	XX	WPI, 1997-154209/14.
XX	XX	
PT	XX	Nucleic acids encoding cellular inhibitor of apoptosis proteins
XX	XX	useful for apoptosis regulation in cells to reduce or increase
PT	XX	apoptosis and for pharmacological screening

XX PS Claim 3; Page 24; 35pp; English.

XX CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -

CC AAT61590/T61591) comprise a series of defined structural domain

CC repeats and/or a RING finger domain; in particular, at least two of

CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat

CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)

CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus

CC sequences derived from these human genes.

CC The nucleic acid is used for recombinant prodn. of human cellular

CC inhibitor of apoptosis protein which modulates apoptosis

CC regulation. The nucleic acids are useful in therapies where

CC increased cell-specific apoptosis is desired, e.g. in restinosis,

CC inflammatory disease states, myocardial infarction, glomerular

CC nephritis, transplant rejection and infectious diseases, e.g. HIV.

CC They can also be used in conditions requiring a reduction in

CC apoptosis.

CC SQ Sequence 55 AA;

Query Match 100.0%; Score 308; DB 18; Length 55;

Best Local Similarity 100.0%; Pred. No. 1.1e-34;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRSTSTFPAGVPVSESLARAGFYTGVDKVCFCGCLMDNWKRGDSP 55

DB 1 CELYRSTSTFPAGVPVSESLARAGFYTGVDKVCFCGCLMDNWKRGDSP 55

RESULT 2

AAW19747

ID AAW19747 standard; Protein; 604 AA.

XX AC AAW19747;

XX DT 16-SEP-1997 (first entry)

XX DE Human inhibitor of apoptosis protein homologue MHC.

XX KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MHC;

KW degenerative disease; infectious disease; autoimmune disease;

KW cancer; therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 29..97

FT /label= BIR

FT Region 169..236

FT /label= BIR

FT Region 255..323

FT /label= BIR

FT Region 536..593

FT /label= RING_finger

XX PN WO9723501-A1.

XX PD 03-JUL-1997.

XX PF 20-DEC-1996; 96WO-AU00827.

XX PR 22-DEC-1995; 95AU-0007275.

XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX PI Vaux DL;

XX DR WPI; 1997-350966/32.

DR N-PSDB; AAT72712.

XX PT Isolated protein homologues of viral inhibitors of apoptosis - used

PT to modulate apoptosis for treatment of degenerative, infectious or

PT autoimmune diseases and cancer

XX PS Claim 9; Page 58-62; 136pp; English.

XX CC Mammalian IAP homologue C (MHC) (AAW19747) is a human homologue of

CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid

CC sequence was deduced from a cDNA clone (see also AAT72712) isolated

CC from a human foetal liver cDNA library using primers based on

CC human EST sequences that resembled the BIR repeats of Orygia

CC pseudotsugata polyhedrosis virus IAP. IAP homologues (see also

CC AAW19745-46 and AAW19748-52) and their derivatives and chemical

CC analogues can be used in methods for modulating apoptosis in animal

CC cells, specifically for treatment, by inhibition, of degenerative

CC and infectious disease or, by promotion, of cancer and autoimmune

CC disease.

CC SQ Sequence 604 AA;

Query Match 100.0%; Score 308; DB 18; Length 604;

Best Local Similarity 100.0%; Pred. No. 1.7e-33;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRSTSTFPAGVPVSESLARAGFYTGVDKVCFCGCLMDNWKRGDSP 55

DB 28 CELYRSTSTFPAGVPVSESLARAGFYTGVDKVCFCGCLMDNWKRGDSP 82

RESULT 3

AAW19582

ID AAW19582 standard; Protein; 604 AA.

XX AC AAW19582;

XX DT 02-SEP-1997 (first entry)

XX DE Human apoptosis inhibitor HIAP-1.

XX KW Apoptosis inhibitor; HIAP-1; HIV; AIDS; neurodegeneration;

KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;

KW reperfusion injury; toxin-induced liver disease; gene therapy;

KW diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 29..96

FT /label= BIR-1

FT Domain 169..235

FT /label= BIR-2

FT Domain 255..322

FT /label= BIR-3

FT Domain 546..591

FT /label= Ring_zinc_finger

XX PN WO9706255-A2.

XX PD 20-FEB-1997.

XX PF 05-AUG-1996; 96WO-IB01022.

XX PR 22-DEC-1995; 95US-0576956.

XX PR 04-AUG-1995; 95US-0511485.

XX PA (UYOT-) UNIV OTTAWA.

XX PI Baird S, Korneluk R, Liston P, Mackenzie AE;

XX DR WPI; 1997-154262/14.

DR N-PSDB; AAT70837.

XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used

PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection

PT of susceptibility to apoptotic disease

XX Claim 27; Page 72-74; 219pp; English.
PS
XX
CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterized by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The HIAP amino acid sequences were deduced from cDNA clones (AAW70837
CC and AAW70838) from a human liver library. IAP polypeptides can be
CC expressed in host cells (in vitro or in vivo) and used in methods
CC for treating diseases and disorders involving apoptosis, esp. in a
CC human diagnosed as HIV-positive or as having AIDS, a
CC neurodegenerative disease, a myelodysplastic syndrome or an
CC ischemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease.
CC
XX
SQ Sequence 604 AA;

Query Match 100.0%; Score 308; DB 18; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRMSTSTFPAGVPYSESLARAGFYTGVDKVKCFCCGLMDNWKRGDSP 55
DB 28 CELYRMSTSTFPAGVPYSESLARAGFYTGVDKVKCFCCGLMDNWKRGDSP 82

RESULT 4
AAW13546
ID AAW13546 standard; Protein; 604 AA.

XX AAW13546;

DT 22-JUL-1997 (first entry)

DE Human c-IAP2.

KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;
KM myocardial infarction; nephritis; HIV.

XX Homo sapiens.

PN WO9706182-A1.

PD 20-FEB-1997.

PF 06-AUG-1996; 96WO-0512860.

PR 08-DEC-1995; 95US-0569749.

PR 08-AUG-1995; 95US-0512946.

XX (TULA-) TULARIK INC.

PI Goeddel DV, Rothe M;

DR WPI; 1997-154209/14.

DR N-PSDB; AAT61591.

PT Nucleic acids encoding cellular inhibitor of apoptosis proteins
PT useful for apoptosis regulation in cells to reduce or increase
PT apoptosis and for pharmacological screening

PS Disclosure; Page 21-23; 35pp; English.

XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2
CC AAW61590/T61591) comprise a series of defined structural domain
CC repeats and/or a RING finger domain; in particular, at least two of
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
CC sequences derived from these human genes.
CC The nucleic acid is used for recombinant prodn. of human cellular

CC inhibitor of apoptosis protein which modulates apoptosis
CC regulation. The nucleic acids are useful in therapies where
CC increased cell-specific apoptosis is desired, e.g. in restinosis,
CC inflammatory disease states, myocardial infarction, glomerular
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC They can also be used in conditions requiring a reduction in
CC apoptosis.
CC
XX
SQ Sequence 604 AA;

Query Match 100.0%; Score 308; DB 18; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRMSTSTFPAGVPYSESLARAGFYTGVDKVKCFCCGLMDNWKRGDSP 55
DB 28 CELYRMSTSTFPAGVPYSESLARAGFYTGVDKVKCFCCGLMDNWKRGDSP 82

RESULT 5
AAW69295
ID AAW69295 standard; Protein; 604 AA.

XX AAW69295;

DT 13-NOV-1998 (first entry)

DE Human HIAP-1 protein.

KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KM proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein.

XX Homo sapiens.

PN WO9635693-A2.

PD 20-AUG-1998.

PF 13-FEB-1998; 98WO-IB00781.

PR 13-FEB-1997; 97US-0800929.

XX (UYOT-) UNIV OTTAWA.

PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;

PI Tsang B;

DR WPI; 1998-467164/40.

DR N-PSDB; AAV55039.

PT Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations

PS Disclosure; Fig 2; 147pp; English.

XX This sequence is the human HIAP-1 protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.


```
XX Human; antisense; inhibitor of apoptosis; XIAP1, XIAP2, XIAP;
KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic disorder; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX Homo sapiens.
OS MO200226968-A2.
PN PD
XX 04-APR-2002.
PD PF
XX 27-SEP-2001; 2001WO-CA01379.
PR PR
XX 28-SEP-2000; 2000US-0672717.
PA PA
XX (UYOT-) UNIV OTTAWA.
XX (AEGE-) AEGERA THERAPEUTICS INC.
PI PI
XX Korneiluk RG, Lacasse E, Baird S, Holcik M, Young S;
DR DR
XX WPI: 2002-479562/51.
DR N-PADB; ABK93870.
XX PT
XX Novel antisense inhibitor of apoptosis nucleic acid useful for
PT enhancing apoptosis in a cell, for treating cancer and other
PT proliferative diseases
XX PS
PS Disclosure; Fig 2; 135pp; English.
XX CC
CC The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse
CC or human XIAP, HIAP1 or HIAP2. Also included are pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis), autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC protein sequence.
XX SQ
XX Sequence 604 AA:
SQ
Query Match 100.0%; Score 308; DB 23 Length 604;
Best Local Similarity 100.0%; Pred. No. 17e-33:
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy 1 CELYRMSTYSTPPAGVPVSESLARAGFYTTGVNDKVVCFCCLMLDNNKRGDSP 55
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 28 CELYRMSTYSTPPAGVPVSESLARAGFYTTGVNDKVVCFCCLMLDNNKRGDSP 82
RESULT 9
ID AAU97837 standard; Protein; 1140 AA.
AC AAU97837;
XX AC
XX DT
XX 27-AUG-2002 (first entry)
DE Human cysteine protease fusion protein AP12-MLT (CPG2).
KM Cysteine protease; CPG2; cell-cell adhesion; lymphoma; osteoporosis;
```

KW rheumatoid arthritis; inflammatory disease; irritable bowel disease;
 KW respiratory disease; asthma; autoimmune disease; bone disease;
 KW atherosclerosis; neoplastic disease; melanoma; prostate; lung tumour;
 KW ovary tumour; myeloproliferative disorder; leukaemia; metastasis;
 KW heart disease; myocardial infarction; cardiac failure; Ap12-MLT;
 KW reperfusion injury; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; neurological disorder; stroke; muscular dystrophy;
 KW liver disease; cataract; infection; transgenic animal; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200233058-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 22-OCT-2001; 2001WO-GB04698.
 XX
 PR 20-OCT-2000; 2000GB-0025816.
 XX
 PR 29-JAN-2001; 2001GB-0002260.
 XX
 PA (INPH-) INPHARMATICA LTD.
 XX
 PI Fagan RJ, Phelps CB, Gutteridge A, Nicholls RQ;
 XX
 DR WPI: 2002-463311/49.
 XX
 DR N-PSDB; ABR52387.
 XX
 PT New proteins identified as cysteine proteases for diagnosing,
 PT preventing and treating neoplastic, inflammatory, autoimmune diseases
 PT and neurological disorders -
 XX
 PS Claim 1; Fig 15; 129pp; English.
 XX
 CC This sequence represents a polypeptide (I) termed BA83099.1 (CPG1),
 CC AAD46161.1 (CPG2) or AAD38507.2 (CPG3), identified as a cysteine
 CC protease, its fragment having cysteine protease activity or having an
 CC antigenic determinant in common with the polypeptide, or its functional
 CC equivalent. (I) is useful as a cysteine protease and for effecting
 CC cell-cell adhesion. A nucleic acid (II) encoding (I) is useful for
 CC expressing a protein that possesses cysteine protease activity. (I),
 CC (II), a vector (III) comprising (II), a ligand (IV) which binds (I) and
 CC a compound (V) that alters the activity of (I), are useful for treating
 CC diseases in which the expression of the natural gene or the activity of
 CC the polypeptide is higher or lower in a diseased patient when compared
 CC to the level of expression or activity in a healthy patient. (I) - (V)
 CC are useful in therapy or diagnosis of disease and in the manufacture of
 CC a medicament for treating lymphoma, rheumatoid arthritis, osteoporosis,
 CC inflammatory disease, such as irritable bowel disease, respiratory
 CC disease such as asthma, autoimmune disease, bone disease,
 CC atherosclerosis, neoplastic diseases, such as melanoma, prostate, lung
 CC and ovary tumours, myeloproliferative disorder, leukaemia, metastasis,
 CC heart disease, myocardial infarction, cardiac failure, reperfusion
 CC injury, neurodegenerative diseases such as Alzheimer's disease,
 CC Parkinson's disease, neurological disorder, stroke, muscular dystrophy,
 CC liver disease, cataract, infection such as bacterial, parasitic,
 CC Plasmodium and viral infection. A transgenic or knockout non-human animal
 CC is useful as an animal model to screen for a compound effective to treat
 CC a disease. This sequence encodes cysteine protease fusion protein
 CC AP12-MLT (CPG2) described in the invention.
 XX
 SQ Sequence 1140 AA;
 XX
 QY Query Match 100.0%; Score 308; DB 23; Length 1140;
 Db Best Local Similarity 100.0%; Pred. No. 3, 6e-33;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CELYRMSTYSTFPAGVPSERSLARAGFYTYGVNDKYKCFCCGLMLDNMKRGDSP 55
 |||
 28 CELYRMSTYSTFPAGVPSERSLARAGFYTYGVNDKYKCFCCGLMLDNMKRGDSP 82

```

ID AAB50694 standard; Protein: 1141 AA.
XX
AC AAB50694;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human API2-MLT chimeric protein sequence.
XX
KW Human; API2-MLT chimera; chimeric; apoptosis inhibitor 2; MLT; API2;
KW mucosa-associated lymphoid tissue lymphoma associated translocation;
KW chromosome 11 region q21-22.3; chromosome 18 region q21.1-22;
KW molecular characterisation; chromosome translocation; carcinogenesis;
KW fusion protein; malignancy.
XX
OS Chimeric - Homo sapiens.
XX
PN WO200073500-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-EP04796.
XX
PR 27-MAY-1999; 99EP-0201683.
XX
PA (VLA-) VLAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Baens M, Marynen P, Dierlamm J;
XX
DR WPI: 2001-061556/07.
DR N-PSDB; AAC90972.
XX
PT Determining if a tissue sample has a chromosome (11:18) translocation
PT associated with malignancies by amplifying a nucleic acid sample using
PT primers complementary to chromosome 11 region q21-22.3 and chromosome
PT 18 region q21.1-22.
XX
PS Claim 12; Fig 5; 47pp; English.
XX
CC The present invention describes a method for determining if a tissue
CC sample comprises a cell with a chromosome (11:18) translocation
CC associated with malignancies such as mucosa-associated lymphoid tissue,
CC (MALT) lymphomas. The method comprises subjecting a sample nucleic acid
CC to amplification using primers complementary to sequences which are on
CC chromosome 11 region q21-22.3 and on chromosome 18 region q21.1-22. The
CC method can be used for determining if a tissue sample or analogue
CC comprises a chromosome (11:18) translocation associated with malignancies
CC such as mucosa-associated lymphoid tissue lymphomas. The nucleic acid or
CC the antibody may be used as a probe for detection, for hybridisation to
CC southern blot cell DNA or for in situ hybridisation of cells, or for
CC determining the presence of complementary DNA. The present sequence
CC represents the specifically claimed chimeric human apoptosis inhibitor 2
CC (API2)/MALT-lymphoma associated translocation (MLT) protein.
XX
SQ Sequence 1141 AA;
XX
Query Match 100.0%; Score 308; DB 2; Length 1141;
Best Local Similarity 100.0%; Pred. No. 3.6e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCFCCGMLDMNKRGDSP 55
DB 28 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCFCCGMLDMNKRGDSP 82
XX
RESULT 11
AAW13547
ID AAW13547 standard; Protein: 55 AA.
XX
AC AAW13547;
XX
DT 22-JUL-1997 (first entry)
XX

```

```

DE Human c-IAP1 repeat 1.
XX
KW IAP; inhibitor; apoptosis; RING finger domain; restinosis;
KW myocardial infarction; nephritis; HIV.
XX
OS Homo sapiens.
XX
PN WO9706182-A1.
XX
PD 20-FEB-1997.
XX
PF 06-AUG-1996; 96WO-US12860.
XX
PR 08-DEC-1995; 95US-0569749.
PR 08-AUG-1995; 95US-0512946.
XX
PA (TULA-) TULARIK INC.
XX
PI Goeddel DV, Rothe M;
XX
DR WPI: 1997-154209/14.
XX
PT Nucleic acids encoding cellular inhibitor of apoptosis proteins
PT useful for apoptosis regulation in cells to reduce or increase
PT apoptosis and for pharmacological screening
XX
PS Claim 3; Page 23; 35pp; English.
XX
CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
CC AAT61590/T61591) comprise a series of defined structural domain
CC repeats and/or a RING finger domain; in particular, at least two of
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
CC sequences derived from these human genes.
CC The nucleic acid is used for recombinant prodn. of human cellular
CC inhibitor of apoptosis protein which modulates apoptosis
CC regulation. The nucleic acids are useful in therapies where
CC increased cell-specific apoptosis is desired, e.g. in restinosis,
CC inflammatory disease states, myocardial infarction, glomerular
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC They can also be used in conditions requiring a reduction in
CC apoptosis.
XX
SQ Sequence 55 AA;
XX
Query Match 97.7%; Score 301; DB 18; Length 55;
Best Local Similarity 98.2%; Pred. No. 1e-33;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCFCCGMLDMNKRGDSP 55
DB 1 CELYRMSTYSTFPAGVPSERSLARAGFYTGVDKVKCFCCGMLDMNKRGDSP 55
XX
RESULT 12
AAU02925
ID AAU02925 standard; Protein: 306 AA.
XX
AC AAU02925;
XX
DT 12-SEP-2001 (first entry)
XX
DE Angiotensin converting enzyme (ACEV) splice variant protein #25.
XX
KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
XX

```

KW nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
 KM vascular disorder; asbestosis.
 XX Homo sapiens.
 OS
 XX
 PN WO200136632-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-IL00766.
 XX
 PR 17-NOV-1999; 99IL-0132978.
 PR 10-DEC-1999; 99IL-0133455.
 XX
 PA (COMP-) COMPUGEN LTD.
 PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 XX WPI; 2001-336004/35.
 DR N-PSDB; AAS06025.
 XX
 PT Novel alternative splicing variants e.g. variant of angiotensin
 PT converting enzyme (ACEV), useful in identifying candidate compounds
 PT capable of binding to the variant and to detect anti-variant antibodies
 PT
 PS
 XX
 PS Claim 4; Fig 25; 519pp; English.
 CC The sequence represents an angiotensin converting enzyme splice variant
 CC (ACEV) polypeptide. The polypeptides of the invention include variants of
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
 CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
 CC polypeptide receptor 2. The polypeptides and their associated nucleic
 CC acids are useful for identification of variant sequences and detection of
 CC candidate compounds capable of binding the molecules. The sequences of
 CC the invention can be used in the treatment and diagnosis of various
 CC disorders including cardiovascular diseases such as arteriosclerosis,
 CC myocardial infarction and coronary arterial thrombosis, renal diseases
 CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC immune disorders such as immune complex nephritis, multiple sclerosis,
 CC cancer, sarcoidosis, nonaroidotic pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis.
 CC
 XX
 SQ Sequence 306 AA;
 Query Match 97.7%; Score 301; DB 22; Length 306;
 Best Local Similarity 98.2%; Pred. No. 7.2e-33;
 Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CELYRMSTYSPAGVPVSESLARAGFYTGVDKVKCFCCGIMLDWKKRGDSP 55
 DB 45 CELYRMSTYSPAGVPVSESLARAGFYTGVDKVKCFCCGIMLDWKKRGDSP 99
 RESULT 13
 AAM19746
 ID AAM19746 standard; Protein; 618 AA.
 XX
 AC AAM19746;
 XX
 DT 16-SEP-1997 (first entry)
 XX
 DE Human inhibitor of apoptosis protein homologue MIHB.
 XX
 KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHB;
 KW degenerative disease; infectious disease; autoimmune disease;
 KW cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT Region 46..113
 FT /label= BIR
 FT Region 184...250
 FT /label= BIR
 FT Region 269...337
 FT /label= BIR
 FT Region 569...606
 FT /label= RING_finger
 XX
 PN WO9723501-A1.
 XX
 PD 03-JUL-1997.
 XX
 PR 20-DEC-1996; 96WO-AU00827.
 XX
 PR 22-DEC-1995; 95AU-0007275.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Vaux DL;
 XX
 DR WPI; 1997-350966/32.
 DR N-PSDB; AAT72711.
 XX
 PT Isolated protein homologues of viral inhibitors of apoptosis - used
 PT to modulate apoptosis for treatment of degenerative, infectious or
 PT autoimmune diseases and cancer
 PT
 PS
 XX
 PS Claim 8; Page 51-54; 136pp; English.
 CC Mammalian IAP homologue B (MIHB) (AAM19746) is a human homologue of
 CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
 CC sequence was deduced from a cDNA clone (see also AAT72711) isolated
 CC from a human foetal liver cDNA library using primers based on
 CC human EST sequences that resembled the BIR repeats of Oryz1.
 CC pseudotsugita polyhedrosis virus IAP. IAP homologues (see also
 CC AAM19745 and AAM19747-52) and their derivatives and chemical analogues
 CC can be used in methods for modulating apoptosis in animal cells,
 CC specifically for treatment, by inhibition, of degenerative and
 CC infectious disease or, by promotion, of cancer and autoimmune
 CC disease.
 CC
 XX
 SQ Sequence 618 AA;
 Query Match 97.7%; Score 301; DB 18; Length 618;
 Best Local Similarity 98.2%; Pred. No. 1.6e-32;
 Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CELYRMSTYSPAGVPVSESLARAGFYTGVDKVKCFCCGIMLDWKKRGDSP 55
 DB 45 CELYRMSTYSPAGVPVSESLARAGFYTGVDKVKCFCCGIMLDWKKRGDSP 99
 RESULT 14
 AAM19583
 ID AAM19583 standard; Protein; 618 AA.
 XX
 AC AAM19583;
 XX
 DT 02-SEP-1997 (first entry)
 XX
 DE Human apoptosis inhibitor HIAP-2.
 XX
 KW Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration;
 KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;
 KW reperfusion injury; toxin-induced liver disease; gene therapy;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 46..113
 FT /label= BIR-1

```
FT Domain 184..250
FT /label= BIR-2
FT 269..336
FT /label= BIR-3
FT 560..605
FT /label= Ring_zinc_finger
XX
XX WO9706255-A2.
XX
XX 20-FEB-1997.
XX
XX 05-AUG-1996; 96WO-IB01022.
XX
XX 22-DEC-1995; 95US-0576956.
XX 04-AUG-1995; 95US-0511485.
XX
XX (UYOT-) UNIV OTTAWA.
XX
XX Baird S, Korneluk RG, Iliston P, Mackenzie AE;
XX
XX WPI, 1997-154262/14.
XX N-PSDB; AAT70838.
XX
XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
XX to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
XX of susceptibility to apoptotic disease
XX
XX Claim 27; Page 75-77; 219pp; English.
XX
XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
XX M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
XX are inhibitors of apoptosis (IAP) and which are characterised by
XX the presence of a ring zinc finger domain (see also AAW19587) and at
XX least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
XX The HIAP amino acid sequences were deduced from cDNA clones (AAT70837
XX and AAT70838) from a human liver library. IAP polypeptides can be
XX expressed in host cells (in vitro or in vivo) and used in methods
XX for treating diseases and disorders involving apoptosis, esp. in a
XX human diagnosed as HIV-positive or as having AIDS, a
XX neurodegenerative disease, a myelodysplastic syndrome or an
XX ischaemic injury, selected from myocardial infarction, stroke,
XX reperfusion injury, or a toxin-induced liver disease.
XX
XX Sequence 618 AA:
SQ
Query Match 97.7%; Score 301; DB 18; Length 618;
Best Local Similarity 98.2%; Pred. No. 1.6e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CELYRMSTYSTPPAGVPSERSLARAGFYTGNDKVKCFCCGLMDNMRGDSF 55
DB 45 CELYRMSTYSTPPAGVPSERSLARAGFYTGNDKVKCFCCGLMDNMRKLGDSF 99
RESULT 15
AAW13545
ID AAW13545 standard; Protein; 618 AA.
AC AAW13545;
XX
XX 22-JUL-1997 (first entry)
XX
XX Human c-IAP1.
XX
XX IAP; inhibitor; apoptosis; RING finger domain; restinosis;
XX myocardial infarction; nephritis; HIV.
XX
XX Homo sapiens.
XX
XX W09706182-A1.
XX
XX 20-FEB-1997.
XX
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PF 06-AUG-1996; 96WO-US12860.
XX
XX 08-DEC-1995; 95US-0569749.
XX 08-AUG-1995; 95US-0512946.
XX
XX (TULA-) TULARIK INC.
XX
XX Goeddel DV, Rothe M;
XX
XX WPI, 1997-154209/14.
XX N-PSDB; AAT61590.
XX
XX Nucleic acids encoding cellular inhibitor of apoptosis proteins -
XX useful for apoptosis regulation in cells to reduce or increase
XX apoptosis and for pharmacological screening
XX
XX Disclosure; Page 18-20; 35pp; English.
XX
XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
XX AAT61590/T61591) comprise a series of defined structural domain
XX repeats and/or a RING finger domain; in particular, at least two of
XX a first domain repeat (AAW13547 or AAW13548), a second domain repeat
XX (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
XX and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
XX sequences derived from these human genes.
XX The nucleic acid is used for recombinant prodn. of human cellular
XX inhibitor of apoptosis protein which modulates apoptosis
XX regulation. The nucleic acids are useful in therapies where
XX increased cell-specific apoptosis is desired, e.g. in restinosis,
XX inflammatory disease states, myocardial infarction, glomerular
XX nephritis, transplant rejection and infectious diseases, e.g. HIV.
XX They can also be used in conditions requiring a reduction in
XX apoptosis.
XX
XX Sequence 618 AA:
SQ
Query Match 97.7%; Score 301; DB 18; Length 618;
Best Local Similarity 98.2%; Pred. No. 1.6e-32;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CELYRMSTYSTPPAGVPSERSLARAGFYTGNDKVKCFCCGLMDNMRGDSF 55
DB 45 CELYRMSTYSTPPAGVPSERSLARAGFYTGNDKVKCFCCGLMDNMRKLGDSF 99
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Search completed: May 5, 2003, 16:01:59
Job time : 11.8353 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:59:02 ; Search time 3.12673 Seconds

(without alignments)
432.866 Million cell updates/sec

Title: US-08-569-749-8

Sequence: 1 LAKAGFYITGPDVACFCAC.....WEIKNDAMSEHLRHPKCPF 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267	100.0	46	US-08-569-749-8	Sequence 8, Appli
2	267	100.0	46	PCR-US96-12860-8	Sequence 8, Appli
3	267	100.0	604	US-08-569-749-4	Sequence 4, Appli
4	267	100.0	604	PCR-US96-12860-4	Sequence 4, Appli
5	264	98.9	67	US-08-511-485-22	Sequence 22, Appli
6	264	98.9	604	US-09-212-971-6	Sequence 6, Appli
7	264	98.9	604	US-08-800-929A-6	Sequence 6, Appli
8	264	98.9	604	US-08-800-929A-6	Sequence 6, Appli
9	264	98.9	604	US-08-569-749-7	Sequence 6, Appli
10	248	92.9	46	US-08-569-749-7	Sequence 7, Appli
11	248	92.9	46	PCR-US96-12860-7	Sequence 7, Appli
12	248	92.9	67	US-08-511-485-23	Sequence 23, Appli
13	248	92.9	438	PCR-US95-05922A-2	Sequence 2, Appli
14	248	92.9	618	US-08-511-485-8	Sequence 8, Appli
15	248	92.9	618	US-09-212-971-8	Sequence 8, Appli
16	248	92.9	618	US-08-800-929A-8	Sequence 8, Appli
17	248	92.9	618	US-08-569-749-2	Sequence 2, Appli
18	248	92.9	618	US-09-069-023-29	Sequence 29, Appli
19	248	92.9	618	US-09-069-023-29	Sequence 2, Appli
20	248	92.9	618	PCR-US96-12860-2	Sequence 2, Appli
21	247	92.5	612	US-09-212-971-14	Sequence 14, Appli
22	247	92.5	612	US-08-800-929A-14	Sequence 14, Appli
23	247	92.5	612	US-08-569-749-14	Sequence 14, Appli
24	247	92.5	612	US-09-617-053A-14	Sequence 14, Appli
25	247	92.5	612	PCR-US96-12860-14	Sequence 14, Appli
26	235	88.0	600	US-09-212-971-12	Sequence 12, Appli
27	235	88.0	600	US-08-800-929A-12	Sequence 12, Appli

28	235	88.0	600	US-09-617-053A-12	Sequence 12, Appli
29	182	68.2	68	US-08-511-485-21	Sequence 21, Appli
30	182	68.2	497	US-08-511-485-4	Sequence 4, Appli
31	182	68.2	497	US-09-212-971-4	Sequence 4, Appli
32	182	68.2	497	US-08-800-929A-4	Sequence 4, Appli
33	182	68.2	497	US-09-617-053A-4	Sequence 4, Appli
34	177	66.3	68	US-08-511-485-20	Sequence 20, Appli
35	177	66.3	496	US-08-511-485-10	Sequence 10, Appli
36	177	66.3	496	US-09-212-971-10	Sequence 10, Appli
37	177	66.3	496	US-08-800-929A-10	Sequence 10, Appli
38	177	66.3	496	US-09-617-053A-10	Sequence 10, Appli
39	145	54.3	67	US-08-511-485-15	Sequence 15, Appli
40	145	54.3	236	US-09-121-979-4	Sequence 4, Appli
41	145	54.3	236	US-09-332-319-4	Sequence 4, Appli
42	145	54.3	236	US-09-239-867-2	Sequence 2, Appli
43	145	54.3	498	US-08-511-485-13	Sequence 13, Appli
44	141	52.8	66	US-08-511-485-25	Sequence 25, Appli
45	141	52.8	236	US-09-239-867-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-569-749-8
Sequence 8, Application US/08569749
Patent No. 6187557

GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goedel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: FLHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)398-3249
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-8

Query Match 100.0%; Score 267; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e-28;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDVACFCACGKLSNWEKNDAMSEHLRHPKCPF 46
DB 1 LAKAGFYITGPDVACFCACGKLSNWEKNDAMSEHLRHPKCPF 46

RESULT 2
PCT-US96-12860-8
Sequence 8, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-8

Query Match 100.0%; Score 267; DB 5; Length 46;
Best local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
Db 1 LAKAGFYIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46

RESULT 3
US-08-569-749-4
Sequence 4, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-4

Query Match 100.0%; Score 267; DB 4; Length 604;
Best local Similarity 100.0%; Pred. No. 3.6e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
Db 189 LAKAGFYIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 234

RESULT 4
PCT-US96-12860-4
Sequence 4, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-4

Query Match 100.0%; Score 267; DB 5; Length 604;
Best local Similarity 100.0%; Pred. No. 3.6e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
DB 189 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 234

RESULT 5

US-08-511-485-22
Sequence 22, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-22

Query Match 98.9%; Score 264; DB 2; Length 67;
Best Local Similarity 97.8%; Pred. No. 7, 9e-28;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
DB 21 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 66

RESULT 6

US-08-511-485-6
Sequence 6, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF SEQUENCES: 38
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-6

Query Match 98.9%; Score 264; DB 2; Length 604;
Best Local Similarity 97.8%; Pred. No. 8, 8e-27;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
DB 189 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 234

RESULT 7

US-09-212-971-6
Sequence 6, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Pratt, Christine
APPLICANT: Tsang, Benjamin K
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 604
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-6

Query Match 98.9%; Score 264; DB 3; Length 604;
Best Local Similarity 97.8%; Pred. No. 8, 8e-27;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 189 LARAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 234

RESULT 8

US-08-800-929A-6
Sequence 6, Application US/08800929A
Patent No. 6133437

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter

APPLICANT: Tsang, Stephen
APPLICANT: Benjamin K
APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elding LLP
STREET: 176 Federal Street
CITY: Boston

STATE: MA
COUNTRY: USA

ZIP: 02110
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A

FILING DATE: 13-FEB-1997
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590

FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354

FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:

NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045

TELEX:
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids

TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-800-929A-6

Query Match 98.9%; Score 264; DB 4; Length 604;
Best local Similarity 97.8%; Pred. No. 8.8e-27;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 189 LARAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 234

RESULT 9

US-09-617-053A-6
Sequence 6, Application US/09617053A
Patent No. 6300492

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter

APPLICANT: Tsang, Stephen
APPLICANT: Benjamin K
APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003

CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13

NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 6
LENGTH: 604

TYPE: PRT
ORGANISM: Homo sapiens

US-09-617-053A-6

Query Match 98.9%; Score 264; DB 4; Length 604;
Best local Similarity 97.8%; Pred. No. 8.8e-27;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 189 LARAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 234

RESULT 10

US-08-569-749-7
Sequence 7, Application US/08569749
Patent No. 6187557

GENERAL INFORMATION:

APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749

FILING DATE:
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.

REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989

TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids

TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-569-749-7
Query Match 92.9%; Score 248; DB 4; Length 46;

Best Local Similarity 91.3%; Pred. No. 6.6e-26;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46
DB 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46

RESULT 11
PCT-US96-12860-7

Sequence 7, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-7

Query Match 92.9%; Score 248; DB 5; Length 46;
Best Local Similarity 91.3%; Pred. No. 6.6e-26;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46
DB 1 LARAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46

RESULT 12
US-08-511-485-23

Sequence 23, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-23

Query Match 92.9%; Score 248; DB 2; Length 67;
Best Local Similarity 91.3%; Pred. No. 1e-25;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46
DB 21 LARAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 66

RESULT 13
PCT-US95-05922A-2

Sequence 2, Application PC/TUS9505922A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922A
FILING DATE: 11 MAY 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-292
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-05922A-2

Query Match 92.9%; Score 248; DB 5; Length 438;
Best Local Similarity 91.3%; Pred. No. 7.9e-25;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPGDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
||:|||||
Db 24 LARAGFYIIGPGDRVACFACGKLSNWEPKDDAMSEHRRHPNCPF 69

RESULT 14

US-08-511-485-8
Sequence 8, Application US/08511485
Patent No. 5919912

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-8

Query Match 92.9%; Score 248; DB 2; Length 618;
Best Local Similarity 91.3%; Pred. No. 1.2e-24;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPGDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
||:|||||
Db 204 LARAGFYIIGPGDRVACFACGKLSNWEPKDDAMSEHRRHPNCPF 249

RESULT 15
US-09-212-971-8

Sequence 8, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-09-212-971-8

Query Match 92.9%; Score 248; DB 3; Length 618;
Best Local Similarity 91.3%; Pred. No. 1.2e-24;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPGDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
||:|||||
Db 204 LARAGFYIIGPGDRVACFACGKLSNWEPKDDAMSEHRRHPNCPF 249

Search completed: May 5, 2003, 16:09:11
Job time: 4.12673 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:07 ; Search time 5.67051 Seconds

(without alignments)
699.970 Million cell updates/sec

Title: US-08-569-749-8

Perfect score: 267
Sequence: 1 LAKAGFYIIGPDRAVACFAC.....WEIKDNAMSEHLRHPKCPF 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	98.9	67	9 US-09-201-936-22	Sequence 22, Appl
2	264	98.9	604	9 US-09-201-936-6	Sequence 6, Appl
3	264	98.9	604	10 US-09-974-592-6	Sequence 6, Appl
4	259	97.0	306	10 US-09-778-927A-62	Sequence 62, Appl
5	248	92.9	67	9 US-09-201-936-23	Sequence 23, Appl
6	248	92.9	438	1 US-08-464-588-2	Sequence 2, Appl
7	248	92.9	618	9 US-09-201-936-8	Sequence 8, Appl
8	248	92.9	618	10 US-09-974-592-8	Sequence 8, Appl
9	247	92.5	612	10 US-09-974-592-14	Sequence 14, Appl
10	244	91.4	591	9 US-09-201-936-42	Sequence 42, Appl
11	235	88.0	600	10 US-09-974-592-12	Sequence 12, Appl
12	235	88.0	602	9 US-09-201-936-40	Sequence 40, Appl
13	182	68.2	68	9 US-09-201-936-21	Sequence 21, Appl
14	182	68.2	110	9 US-09-965-967-21	Sequence 21, Appl
15	182	68.2	497	9 US-09-201-936-4	Sequence 4, Appl
16	182	68.2	497	10 US-09-974-592-4	Sequence 4, Appl
17	177	66.3	68	9 US-09-201-936-20	Sequence 20, Appl
18	177	66.3	496	9 US-09-201-936-10	Sequence 10, Appl
19	177	66.3	496	10 US-09-974-592-10	Sequence 10, Appl

20	145	54.3	67	9 US-09-201-936-15	Sequence 15, Appl
21	145	54.3	498	9 US-09-201-936-13	Sequence 13, Appl
22	141	52.8	66	9 US-09-201-936-25	Sequence 25, Appl
23	141	52.8	107	9 US-09-965-967-20	Sequence 20, Appl
24	141	52.8	278	9 US-09-964-899-39	Sequence 39, Appl
25	141	52.8	1403	8 US-08-913-322-22	Sequence 22, Appl
26	141	52.8	1403	8 US-08-913-322-24	Sequence 24, Appl
27	140	52.4	66	9 US-09-201-936-24	Sequence 24, Appl
28	136	50.9	68	9 US-09-201-936-27	Sequence 27, Appl
29	135	50.6	68	9 US-09-201-936-28	Sequence 28, Appl
30	135	50.6	68	9 US-10-041-859-18	Sequence 18, Appl
31	135	50.6	172	9 US-10-041-859-12	Sequence 12, Appl
32	132	49.4	68	9 US-09-201-936-19	Sequence 19, Appl
33	131	49.1	68	9 US-09-201-936-18	Sequence 18, Appl
34	131	49.1	68	9 US-09-201-936-29	Sequence 29, Appl
35	131	49.1	68	9 US-10-041-859-17	Sequence 17, Appl
36	131	49.1	172	9 US-10-041-859-11	Sequence 11, Appl
37	131	49.1	275	9 US-09-201-936-12	Sequence 12, Appl
38	130	48.7	68	9 US-10-041-859-19	Sequence 19, Appl
39	129	48.3	68	9 US-09-201-936-26	Sequence 26, Appl
40	129	48.3	109	9 US-09-965-967-30	Sequence 30, Appl
41	129	48.3	172	9 US-10-041-859-13	Sequence 13, Appl
42	127	47.6	68	9 US-10-041-859-14	Sequence 14, Appl
43	127	47.6	172	9 US-10-041-859-8	Sequence 8, Appl
44	127	47.6	346	9 US-10-041-859-2	Sequence 2, Appl
45	126	47.2	68	9 US-10-041-859-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-201-936-22
; Sequence 22, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROOBS, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-22

Query Match 98.9%; Score 264; DB 9; Length 67;
Best Local Similarity 97.8%; Pred. No. 1.7e-26;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRAVACFACGKLSNMEPRDNAMSEHLRHPKCPF 46
||:|||||
Db 21 LAKAGFYIIGPDRAVACFACGKLSNMEPRDNAMSEHLRHPKCPF 66

RESULT 2
US-09-201-936-6
; Sequence 6, Application US/09201936

```
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-6
```

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Query Match          98.9%; Score 264; DB 9; Length 604;
Best Local Similarity 97.8%; Pred. No. 1.9e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 LAKAGFYIIGPGRVACFACGKLSNWEKDNAMSEHLRHFPKCP 46
DB 189 LARAGFYIIGPGRVACFACGKLSNWEKDNAMSEHLRHFPKCP 234
```

```
RESULT 3
US-09-974-592-6
; Sequence 6, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K.
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-6
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Query Match          98.9%; Score 264; DB 10; Length 604;
Best Local Similarity 97.8%; Pred. No. 1.9e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 LAKAGFYIIGPGRVACFACGKLSNWEKDNAMSEHLRHFPKCP 46
DB 189 LARAGFYIIGPGRVACFACGKLSNWEKDNAMSEHLRHFPKCP 234
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```
RESULT 4
US-09-778-927A-62
; Sequence 62, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(306)
; OTHER INFORMATION: xaa - any amino acid, unknown, or other
US-09-778-927A-62
```

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Query Match          97.0%; Score 259; DB 10; Length 306;
Best Local Similarity 95.7%; Pred. No. 3.8e-25;
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 LAKAGFYIIGPGRVACFACGKLSNWEKDNAMSEHLRHFPKCP 46
DB 204 LARAGFYIIGPGRVACFACGKLSNWEKDNAMSEHLRHFPKCP 249
```

```
RESULT 5
US-09-201-936-23
; Sequence 23, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-23
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```
Query Match          92.9%; Score 248; DB 9; Length 67;
Best Local Similarity 91.3%; Pred. No. 1.8e-24;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 LAKAGFYIIGPGRVACFACGKLSNWEKDNAMSEHLRHFPKCP 46
DB 189 LARAGFYIIGPGRVACFACGKLSNWEKDNAMSEHLRHFPKCP 234
```

Db 21 LARAGFYIIGPDRVACFACGKLSNWEKDKDAMSEHRRHFPNCPF 66

RESULT 6
US-08-464-588-2
; Sequence 2, Application US/08464588
; Publication No. US20030073159A1
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,588
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05922
; FILING DATE: 11 MAY 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-387
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-464-588-2

Query Match 92.9%; Score 248; DB 1; Length 438;
Best Local Similarity 91.3%; Pred. No. 1.4e-23;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDKDAMSEHRRHFPNCPF 46
DB 24 LARAGFYIIGPDRVACFACGKLSNWEKDKDAMSEHRRHFPNCPF 69

RESULT 7
US-09-201-936-8
; Sequence 8, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022

EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-8

Query Match 92.9%; Score 248; DB 9; Length 618;
Best Local Similarity 91.3%; Pred. No. 2.1e-23;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDKDAMSEHRRHFPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEKDKDAMSEHRRHFPNCPF 249

RESULT 8
US-09-974-592-8
; Sequence 8, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-8

Query Match 92.9%; Score 248; DB 10; Length 618;
Best Local Similarity 91.3%; Pred. No. 2.1e-23;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDKDAMSEHRRHFPNCPF 46
DB 204 LARAGFYIIGPDRVACFACGKLSNWEKDKDAMSEHRRHFPNCPF 249

RESULT 9
US-09-974-592-14
; Sequence 14, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

```
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-14
```

```
Query Match          92.5%; Score 247; DB 10; Length 612;
Best Local Similarity 91.3%; Pred. No. 2.7e-23;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 197 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 242
```

```
RESULT 10
US-09-201-936-42
; Sequence 42, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-42
```

```
Query Match          91.4%; Score 244; DB 9; Length 591;
Best Local Similarity 91.3%; Pred. No. 6.3e-23;
Matches 42; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 176 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 221
```

```
RESULT 11
US-09-974-592-12
; Sequence 12, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
```

```
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-12
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```
Query Match          88.0%; Score 235; DB 10; Length 600;
Best Local Similarity 89.1%; Pred. No. 9e-22;
Matches 41; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 187 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 232
```

```
RESULT 12
US-09-201-936-40
; Sequence 40, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-201-936-40
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```
Query Match          88.0%; Score 235; DB 9; Length 602;
Best Local Similarity 89.1%; Pred. No. 9e-22;
Matches 41; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 189 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 234
```

```
RESULT 13
US-09-201-936-21
; Sequence 21, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-21
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Query Match          68.2%; Score 182; DB 9; Length 68;
Best Local Similarity 69.6%; Pred. No. 4.5e-16;
Matches 32; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
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OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHRRHFKPCPF 46
Db 22 LASAGLYTYGIGDQVQCFCCGKLNWPCDRAWSEHRRHFKPCPF 67
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```
RESULT 14
US-09-965-967-21
; Sequence 21, Application US/09965967
; Patent No. US2002017557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236,574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256,830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-21
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Query Match          68.2%; Score 182; DB 9; Length 110;
Best Local Similarity 69.6%; Pred. No. 7.6e-16;
Matches 32; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
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```
OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHRRHFKPCPF 46
Db 36 LASAGLYTYGIGDQVQCFCCGKLNWPCDRAWSEHRRHFKPCPF 81
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RESULT 15
US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
```

```
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-4
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```
Query Match          68.2%; Score 182; DB 9; Length 497;
Best Local Similarity 69.6%; Pred. No. 3.9e-15;
Matches 32; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
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```
OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHRRHFKPCPF 46
Db 184 LASAGLYTYGIGDQVQCFCCGKLNWPCDRAWSEHRRHFKPCPF 229
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Search completed: May 5, 2003, 16:11:06
Job time : 6.67051 secs
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```
RESULT 8
AAW19582
ID AAW19582 standard; Protein: 604 AA.
XX
AC AAW19582;
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor HIAP-1.
XX
KM Apoptosis inhibitor; HIAP-1; HIV; AIDS; neurodegeneration;
KW myelodysplastic syndrome; ischemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 29..96
FT Domain /label= BIR-1
FT Domain 169..235
FT Domain /label= BIR-2
FT Domain 255..322
FT Domain /label= BIR-3
FT Domain 546..591
FT Domain /label= Ring_zinc_finger
XX
PN WO9706255-A2.
XX
PD 20-FEB-1997.
XX
PF 05-AUG-1996; 96WO-IB01022.
XX
PR 22-DEC-1995; 95US-0576956.
PR 04-AUG-1995; 95US-0511485.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX
DR WPI: 1997-154262/14.
DR N-PSDB; AAT70837.
XX
PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT of susceptibility to apoptotic disease
XX
PS Claim 27; Page 72-74; 219pp; English.
XX
CC Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterised by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The HIAP amino acid sequences were deduced from cDNA clones (AAT70837
CC and AAT70838) from a human liver library. IAP polypeptides can be
CC expressed in host cells (in vitro or in vivo) and used in methods
CC for treating diseases and disorders involving apoptosis, esp. in a
CC human diagnosed as HIV-positive or as having AIDS, a
CC neurodegenerative disease, a myelodysplastic syndrome or an
CC ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease.
XX
SQ Sequence 604 AA;
XX
Query Match 98.9%; Score 264; DB 18; Length 604;
Best Local Similarity 97.8%; Pred. No. 3.2e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 9
AAW69295
ID AAW69295 standard; Protein: 604 AA.
XX
AC AAW69295;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human HIAP-1 protein.
XX
KM Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 29..96
FT Domain /label= BIR-1
FT Domain 169..235
FT Domain /label= BIR-2
FT Domain 255..322
FT Domain /label= BIR-3
FT Domain 546..591
FT Domain /label= Ring_zinc_finger
XX
PN WO9835693-A2.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-IB00781.
XX
PR 13-FEB-1997; 97US-0800929.
XX
PA (UYOT-) UNIV OTTAWA.
XX
PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
PI Tsang B;
XX
DR WPI: 1998-467164/40.
DR N-PSDB; AAV55039.
XX
PT Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations
XX
PS Disclosure; Fig 2; 147pp; English.
XX
CC This sequence is the human HIAP-1 protein, which is an inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.
XX
SQ Sequence 604 AA;
XX
Query Match 98.9%; Score 264; DB 19; Length 604;
Best Local Similarity 97.8%; Pred. No. 3.2e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
1 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
11:|||||
189 LAKAGFYIIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 234
```

```
RESULT 10
ABG65664
ID ABG65664 standard; Protein: 604 AA.
XX
AC ABG65664;
XX
```

DT 26-AUG-2002 (first entry)
XX
XX Human inhibitor of apoptosis, HIAP1.
DE
XX Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytosolic cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX
XX Homo sapiens.
OS
XX WO200226968-A2.
PN
XX 04-APR-2002.
PD
XX 27-SEP-2001; 2001WO-CA01379.
PF
XX 28-SEP-2000; 2000US-0672717.
PR
XX (UYOT-) UNIV OTTAWA.
PA (AEGE-) AEGERA THERAPEUTICS INC.
XX
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
PI WPI; 2002-479562/51.
DR N-PSDB; ABR93870.
XX
XX Novel antisense inhibitor of apoptosis nucleic acid useful for
PT enhancing apoptosis in a cell, for treating cancer and other
PT proliferative diseases
XX
XX Disclosure; Fig 2; 135pp; English.
PS
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC protein sequence.
XX
XX Sequence 604 AA;
SQ
Query Match 98.9%; Score 264; DB 23; Length 604;
Best Local Similarity 97.8%; Pred. No. 3.2e-25;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPGRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 46
II:|||||
DB 189 LARAGFYIIGPGRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 234

RESULT 11
AAU02925
ID AAU02925 standard; Protein; 306 AA.
XX
AC AAU02925;
XX
DT 12-SEP-2001 (first entry)
XX

DE Angiotensin converting enzyme (ACEV) splice variant protein #25.
XX
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.
XX
XX Homo sapiens.
OS
XX WO200136632-A2.
PN
XX 25-MAY-2001.
PD
XX 17-NOV-2000; 2000WO-IL00766.
PF
XX 17-NOV-1999; 99IL-0132978.
PR 10-DEC-1999; 99IL-0133455.
PR
XX (COMP-) COMPUGEN LTD.
PA
XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
PI WPI; 2001-336004/35.
DR N-PSDB; AAS06025.
XX
XX Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies
XX
XX Claim 4; Fig 25; 519pp; English.
PS
XX The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding to the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis.
XX
XX Sequence 306 AA;
SQ
Query Match 97.0%; Score 259; DB 22; Length 306;
Best Local Similarity 95.7%; Pred. No. 6.7e-25;
Matches 44; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPGRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 46
II:|||||
DB 204 LARAGFYIIGPGRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 249

RESULT 12
AAW13549
ID AAW13549 standard; Protein; 46 AA.
XX
AC AAW13549;
XX
DT 22-JUL-1997 (first entry)
XX

```

XX DE Human c-IAP1 repeat 2.
XX XX IAP; inhibitor of apoptosis; RING finger domain; restinosis;
KW myocardial infarction; nephritis; HIV.
XX OS Homo sapiens.
XX PN WO9706182-A1.
XX PD 20-FEB-1997.
XX PF 06-AUG-1996; 96WO-US12860.
XX PR 08-DEC-1995; 95US-0569749.
XX PR 08-AUG-1995; 95US-0512946.
XX PA (TULA-) TULARIK INC.
XX PI Goeddel DV, Rothe M;
XX DR WPI; 1997-154209/14.
XX XX
XX PT Nucleic acids encoding cellular inhibitor of apoptosis proteins
XX PT useful for apoptosis regulation in cells to reduce or increase
XX PT apoptosis and for pharmacological screening
XX PS Claim 3; Page 24; 35pp; English.
XX XX
CC The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -
CC AAT61590/761591) comprise a series of defined structural domain
CC repeats and/or a RING finger domain; in particular, at least two of
CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat
CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)
CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus
CC sequence derived from these human genes.
CC The nucleic acid is used for recombinant prodn. of human cellular
CC inhibitor of apoptosis protein which modulates apoptosis
CC regulation. The nucleic acids are useful in therapies where
CC increased cell-specific apoptosis is desired, e.g. in restinosis,
CC inflammatory disease states, myocardial infarction, glomerular
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC They can also be used in conditions requiring a reduction in
CC apoptosis.
XX SQ Sequence 46 AA;
XX XX
XX Query Match 92.9%; Score 248; DB 18; Length 46;
XX Best Local Similarity 91.3%; Pred. No. 2.3e-24;
XX Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHHRHFKPCPF 46
Db 1 LARAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHHRHFKPCPF 46
XX XX
RESULT 13
AAW04583
ID AAW04583 standard; Protein; 438 AA.
XX AC AAW04583;
XX DT 07-FEB-1997 (first entry)
XX DE Human inhibitor of apoptosis gene 1.
XX KW Inhibitor of apoptosis 1; hIAP-1; degenerative disease;
KW rheumatoid arthritis; septic shock; antiviral; trauma; stroke;
KW cell death; oncogenesis; cancer; diagnosis; therapy.
XX OS Homo sapiens.
XX PN WO9635703-A1.

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XX PD 14-NOV-1996.
XX XX
XX PE 11-MAY-1995; 95WO-US05922.
XX PR 11-MAY-1995; 95WO-US05922.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI He WW, Hudson PL, Rosen CA;
XX DR WPI; 1996-518608/51.
XX DR N-PSDB; AAT43709.
XX XX
XX PT Polynucleotide encoding human inhibitor of apoptosis gene 1 - useful
XX PT for treating degenerative diseases, as antiviral defence mechanism
XX PT and preventing cell death during trauma and strokes
XX PS Claim 1; Page 40-41; 53pp; English.
XX XX
CC Human inhibitor of apoptosis 1 (hIAP-1) (AAW04583) is a protein
CC useful for treating degenerative diseases, rheumatoid arthritis,
CC septic shock, as an antiviral defence mechanism, and for
CC preventing cell death during strokes or trauma. Its amino acid
CC sequence was deduced from a cDNA clone (AAT43709) that can be obtd.
CC from human Jurkat cell lines or human osteoclastoma stromal cell
CC lines. Recombinant hIAP-1 can be produced in prokaryotic or
CC eukaryotic host cells, or expressed in vivo. It can also be used
CC to screen for modulators of hIAP-1 activity.
XX SQ Sequence 438 AA;
XX XX
XX Query Match 92.9%; Score 248; DB 17; Length 438;
XX Best Local Similarity 91.3%; Pred. No. 2.5e-23;
XX Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHHRHFKPCPF 46
Db 24 LARAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHHRHFKPCPF 69
XX XX
RESULT 14
AAW19746
ID AAW19746 standard; Protein; 618 AA.
XX AC AAW19746;
XX DT 16-SEP-1997 (first entry)
XX DE Human inhibitor of apoptosis protein homologue MIHB.
XX KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHB;
KW degenerative disease; infectious disease; autoimmune disease;
KW cancer; therapy; diagnosis.
XX OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
XX FT Region 46..113
XX FT Region /label= BIR
XX FT Region 184..250
XX FT Region /label= BIR
XX FT Region 269..337
XX FT Region /label= BIR
XX FT Region 569..606
XX FT Region /label= RING_finger
XX PN WO9723501-A1.
XX PD 03-JUL-1997.
XX PF 20-DEC-1996; 96WO-AU00827.
XX XX

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PR 22-DEC-1995; 95AU-0007275.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Vaux DL;
PI
DR WPI; 1997-350966/32.
XX N-PSDB; AAT72711.
XX
XX Isolated protein homologues of viral inhibitors of apoptosis - used
PT to modulate apoptosis for treatment of degenerative, infectious or
PT autoimmune diseases and cancer
XX
XX Claim 8; Page 51-54; 136pp; English.
XX
XX Mammalian IAP homologue B (MIHB) (AAW19746) is a human homologue of
CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
CC sequence was deduced from a cDNA clone (see also AAT72711) isolated
CC from a human foetal liver cDNA library using primers based on
CC human EST sequences that resembled the BIR repeats of Oryzla
CC pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also
CC AAW19745 and AAW19747-52) and their derivatives and chemical analogues
CC can be used in methods for modulating apoptosis in animal cells,
CC specifically for treatment, by inhibition, of degenerative and
CC infectious disease or, by promotion, of cancer and autoimmune
CC disease.
XX
XX Sequence 618 AA;
SQ
Query Match 92.9%; Score 248; DB 18; Length 618;
Best Local Similarity 91.3%; Pred. No. 3.6e-23;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46
DB 204 LAKAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 249
RESULT 15
AAW19583
ID AAW19583 standard; Protein; 618 AA.
XX
XX AAW19583;
AC
XX
DT 02-SEP-1997 (first entry)
XX
DE Human apoptosis inhibitor HIAP-2.
XX
XX Apoptosis inhibitor; HIAP-2; HIV; AIDS; neurodegeneration;
KW myelodysplastic syndrome; ischaemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX FH Domain 46..113
XX FT Domain /label= BIR-1
XX FT Domain 184..250
XX FT Domain /label= BIR-2
XX FT Domain 269..336
XX FT Domain /label= BIR-3
XX FT Domain 560..605
XX FT /label= Ring_zinc_finger
XX
XX WO9706255-A2.
XX
XX 20-FEB-1997.
XX
XX 05-AUG-1996; 96WO-IB01022.
XX
XX 22-DEC-1995; 95US-0576956.
XX
XX 04-AUG-1995; 95US-0511485.
PR

```

```

XX
XX (UYOT-) UNIV OTTAWA.
XX
XX Baird S, Korneluk RG, Liston P, Mackenzie AE;
XX
XX WPI; 1997-154262/14.
XX N-PSDB; AAT70838.
XX
XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
PT of susceptibility to apoptotic disease
XX
XX Claim 27; Page 75-77; 219pp; English.
XX
XX Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and
CC M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that
CC are inhibitors of apoptosis (IAP) and which are characterised by
CC the presence of a ring zinc finger domain (see also AAW19587) and at
CC least one BIR (baculovirus IAP repeat) domain (see also AAW19588).
CC The HIAP amino acid sequences were deduced from cDNA clones (AAT70837
CC and AAT70838) from a human liver library. IAP polypeptides can be
CC expressed in host cells (in vitro or in vivo) and used in methods
CC for treating diseases and disorders involving apoptosis, esp. in a
CC human diagnosed as HIV-positive or as having AIDS, a
CC neurodegenerative disease, a myelodysplastic syndrome or an
CC ischaemic injury, selected from myocardial infarction, stroke,
CC reperfusion injury, or a toxin-induced liver disease.
XX
XX Sequence 618 AA;
SQ
Query Match 92.9%; Score 248; DB 18; Length 618;
Best Local Similarity 91.3%; Pred. No. 3.6e-23;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46
DB 204 LAKAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 249

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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	267	100.0	46	18	AAW13550	Human c-IAP2 repea
2	267	100.0	604	18	AAW19747	Human inhibitor of
3	267	100.0	604	18	AAW13546	Human c-IAP2. Hom
4	267	100.0	604	20	AAW52703	Human cellular inh
5	267	100.0	604	20	AAW33997	Human cellular inh
6	267	100.0	1140	23	AAU97837	Human cysteine pro
7	267	100.0	1141	22	AAW50694	Human API2-MIT chi
8	264	98.9	604	18	AAW19582	Human apoptosis in
9	264	98.9	604	19	AAW69295	Human HIAP-1 prote
10	264	98.9	604	23	ABG65664	Human inhibitor of

11	259	97.0	306	22	AAU02925	Angiotensin conver
12	248	92.9	46	18	AAW13549	Human c-IAP1 repea
13	248	92.9	438	17	AAW04583	Human inhibitor of
14	248	92.9	618	18	AAW19746	Human inhibitor of
15	248	92.9	618	18	AAW19583	Human apoptosis in
16	248	92.9	618	18	AAW13545	Human c-IAP1. Hom
17	248	92.9	618	18	AAW13545	Human c-IAP1. Hom
18	248	92.9	618	20	AAW33998	Human cellular inh
19	248	92.9	618	23	ABG65665	Human inhibitor of
20	247	92.5	612	19	AAW13555	Murine c-IAP. Mus
21	247	92.5	612	19	AAW69299	Murine HIAP-2 prot
22	244	91.4	591	18	AAW19586	Mouse apoptosis in
23	244	91.4	591	23	ABG65668	Mouse inhibitor of
24	235	88.0	600	19	AAW69298	Murine HIAP-1 prot
25	235	88.0	602	18	AAW19585	Mouse apoptosis in
26	235	88.0	602	23	ABG65667	Mouse inhibitor of
27	182	68.2	497	18	AAW19581	Human apoptosis in
28	182	68.2	497	19	AAW69294	Human XIAP protein
29	182	68.2	497	21	AAW99985	Human X-linked inh
30	182	68.2	497	21	AAW99985	Human XIAP protein
31	182	68.2	497	23	ABG65663	Human inhibitor of
32	178	66.7	464	23	AAU75747	Human inhibitor of
33	177	66.3	496	18	AAW19745	Mouse inhibitor of
34	177	66.3	496	18	AAW19584	Mouse apoptosis in
35	177	66.3	496	19	AAW69297	Murine XIAP protei
36	177	66.3	496	23	ABG65666	Mouse inhibitor of
37	145	54.3	236	21	AAW14440	Human TIAP (an inh
38	145	54.3	236	22	AAE00365	Human IAP-like pro
39	145	54.3	236	22	AAE00366	Chimpanzee IAP-lik
40	145	54.3	236	23	AAU75066	Human testes speci
41	145	54.3	498	18	AAW19748	Drosophila inhibit
42	145	54.3	498	22	ABW62863	Drosophila melanog
43	144	53.9	236	22	AAE00367	Gorilla IAP-like p
44	141	52.8	278	23	AAO20511	Protein of APP rel
45	141	52.8	1232	17	AAW98217	Neuronal apoptosis

ALIGNMENTS

RESULT 1	AAW13550	standard; Protein: 46 AA.
ID	AAW13550	
AC	AAW13550;	
XX		
DT	22-JUL-1997 (first entry)	
XX		
DE	Human c-IAP2 repeat 2.	
XX		
KW	IAP; inhibitor; apoptosis; RING finger domain; restinosis;	
XX	myocardial infarction; nephritis; HIV.	
OS	Homo sapiens.	
XX		
PN	WO9706182-A1.	
XX		
PD	20-FEB-1997.	
XX		
PF	06-AUG-1996; 96WO-US12860.	
XX		
PR	08-DEC-1995; 95US-0569749	
PR	08-AUG-1995; 95US-0512946	
XX		
PA	(TULAR-) TULARIK INC.	
XX		
PI	Goeddel DV, Rothe M;	
XX		
DR	WPI; 1997-154209/14.	
XX		
PT	Nucleic acids encoding cellular inhibitor of apoptosis proteins -	
PT	useful for apoptosis regulation in cells to reduce or increase	
PT	apoptosis and for pharmacological screening	

XX Claim 3; Page 24; 35pp; English.

PS The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -

XX AAT61590/761591) comprise a series of defined structural domain

CC repeats and/or a RING finger domain; in particular, at least two of

CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat

CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)

CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus

CC sequences derived from these human genes.

CC The nucleic acid is used for recombinant prodn. of human cellular

CC inhibitor of apoptosis protein which modulates apoptosis

CC regulation. The nucleic acids are useful in therapies where

CC increased cell-specific apoptosis is desired, e.g. in restinosis,

CC inflammatory disease sites, myocardial infarction, glomerular

CC nephritis, transplant rejection and infectious diseases, e.g. HIV.

CC They can also be used in conditions requiring a reduction in

CC apoptosis.

XX

XX Sequence 46 AA;

XX

XX Query Match 100.0%; Score 267; DB 18; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 8.5e-27;

XX Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46

DB 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46

RESULT 2

AAW19747

ID AAW19747 standard; Protein; 604 AA.

XX

XX AAW19747;

XX

XX 16-SEP-1997 (first entry)

XX

XX Human inhibitor of apoptosis protein homologue MHC.

XX

XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MHC;

XX KW degenerative disease; infectious disease; autoimmune disease;

XX cancer; therapy; diagnosis.

XX

XX Homo sapiens.

XX

XX

XX Key Location/Qualifiers

XX FT Region 29..97

XX FT Region /label= BIR

XX FT Region 169..236

XX FT Region /label= BIR

XX FT Region 255..323

XX FT Region /label= BIR

XX FT Region 556..593

XX FT Region /label= RING_finger

XX

XX WO9723501-A1.

XX

XX 03-JUL-1997.

XX

XX 20-DEC-1996; 96WO-AU00827.

XX

XX 22-DEC-1995; 95AU-0007275.

XX

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX

XX Vaux DL;

XX

XX WPI; 1997-350966/32.

XX

XX N-PSDB; AAT72712.

XX

XX Isolated protein homologues of viral inhibitors of apoptosis - used

XX PT to modulate apoptosis for treatment of degenerative, infectious or

PT autoimmune diseases and cancer

XX

XX Claim 9; Page 58-62; 136pp; English.

PS

XX Mammalian IAP homologue C (MHC) (AAW19747) is a human homologue of

XX baculovirus inhibitor of apoptosis protein (IAP). Its amino acid

CC sequence was deduced from a cDNA clone (see also AAT72712) isolated

CC from a human foetal liver cDNA library using primers based on

CC human EST sequences that resembled the BIR repeats of Orygia

CC pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also

CC AAW19745-46 and AAW19748-52) and their derivatives and chemical

CC analogues can be used in methods for modulating apoptosis in animal

CC cells, specifically for treatment, by inhibition, of degenerative

CC and infectious disease or, by promotion, of cancer and autoimmune

CC disease.

XX

XX Sequence 604 AA;

XX

XX Query Match 100.0%; Score 267; DB 18; Length 604;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-25;

XX Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46

DB 189 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 234

RESULT 3

AAW13546

ID AAW13546 standard; Protein; 604 AA.

XX

XX AAW13546;

XX

XX 22-JUL-1997 (first entry)

XX

XX Human c-IAP2.

XX

XX IAP; inhibitor; apoptosis; RING finger domain; restinosis;

XX KW myocardial infarction; nephritis; HIV.

XX

XX Homo sapiens.

XX

XX WO9706182-A1.

XX

XX 20-FEB-1997.

XX

XX 06-AUG-1996; 96WO-US12860.

XX

XX 08-DEC-1995; 95US-0569749.

XX

XX 08-AUG-1995; 95US-0512946.

XX

XX (TULA-) TULARIK INC.

XX

XX Goeddel DV, Rothe M;

XX

XX WPI; 1997-154209/14.

XX

XX N-PSDB; AAT61591.

XX

XX Nucleic acids encoding cellular inhibitor of apoptosis proteins -

XX PT useful for apoptosis regulation in cells to reduce or increase

XX apoptosis and for pharmacological screening

XX

XX Disclosure; Page 21-23; 35pp; English.

XX

XX The human cellular inhibitor of apoptosis proteins (c-IAP1/2 -

XX AAT61590/761591) comprise a series of defined structural domain

CC repeats and/or a RING finger domain; in particular, at least two of

CC a first domain repeat (AAW13547 or AAW13548), a second domain repeat

CC (AAW13549 or AAW13550), and a third domain repeat (AAW13551 or AAW13552)

CC and/or a RING finger domain (AAW13553 or AAW13554), or a consensus

CC sequences derived from these human genes.

CC The nucleic acid is used for recombinant prodn. of human cellular

CC inhibitor of apoptosis protein which modulates apoptosis

CC regulation. The nucleic acids are useful in therapies where
CC increased cell-specific apoptosis is desired, e.g. in restitosis,
CC inflammatory disease states, myocardial infarction, glomerular
CC nephritis, transplant rejection and infectious diseases, e.g. HIV.
CC They can also be used in conditions requiring a reduction in
CC apoptosis.

XX
SQ Sequence 604 AA;

Query Match 100.0%; Score 267; DB 18; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.3e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACACGKLSNWEKDNAMSEHLRHPKCP 46
Db 189 LAKAGFYIIGPDRVACACGKLSNWEKDNAMSEHLRHPKCP 234

RESULT 4
AA52703
ID AAY52703 standard; Protein; 604 AA.
XX
AC AAY52703;
XX
DT 26-JAN-2000 (first entry)
XX
DE Human cellular inhibitor of apoptosis-2 protein.
XX
KW Identification; genetic target; gene modulation; human;
KW antisense oligonucleotide; phosphorothioate; target validation;
KW nucleotide sequence-based technology; antisense drug discovery.
XX
OS Homo sapiens.
XX
PN WO9553101-A1.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99MO-US08268.
XX
PR 13-APR-1998; 98US-0081483.
PR 28-APR-1998; 98US-0067638.
XX
PA (ISIS-) ISIS PHARM INC.
PI Coweart LM, Baker BF, McNeill J, Freiler SM, Sasnor HM, Brooks DG;
PI Ohast C, Wyatt JR, Borchers AH, Vickers TA;
XX
DR WPI: 1999-620446/53.
DR N-PSDB; AA241005.
XX
XX
PT Identifying compounds which modulate expression of nucleic acids, used
PT to provide compounds having defined physical, chemical or bioactive
PT properties, e.g. antisense activity
XX
PS Example 20; Page 197-202; 264pp; English.
XX
XX
CC A method has been developed of defining a set of compounds that modulate
CC the expression of a target nucleic acid (tNA) sequence via binding of
CC the compounds with the tNA sequence. The method comprises generating a
CC library of virtual compounds in silico according to defined criteria,
CC and evaluating in silico the binding of the virtual compounds with the
CC tNA according to defined criteria. Also described are: (1) a method of
CC defining a set of oligonucleotides (ONS) that modulate the expression of
CC a tNA sequence via binding of the ONS with the tNA sequence comprising
CC generating a library of virtual compounds in silico according to defined
CC criteria, and evaluating in silico the binding of the virtual ONS with
CC the tNA according to defined criteria; and (2) a method of defining a
CC set of compounds that modulate the expression of a tNA sequence via
CC binding of the compounds with the tNA. The methods can be used for the
CC generation and identification of synthetic compounds having defined
CC physical, chemical or bioactive properties. Information gathered from
CC assays of such compounds is used to identify nucleic acid sequences that

CC are tractable to a variety of nucleotide sequence-based technologies,
CC e.g. antisense drug discovery and target validation. AA240852 to
CC AA241220, and AAY52701 to AAY52706, represent sequences used in the
CC exemplification of the present invention.

XX
SQ Sequence 604 AA;

Query Match 100.0%; Score 267; DB 20; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.3e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACACGKLSNWEKDNAMSEHLRHPKCP 46
Db 189 LAKAGFYIIGPDRVACACGKLSNWEKDNAMSEHLRHPKCP 234

RESULT 5
AAY33997
ID AAY33997 standard; Protein; 604 AA.
XX
AC AAY33997;
XX
DT 26-NOV-1999 (first entry)
XX
DE Human cellular inhibitor of apoptosis-2 sequence.
XX
KW Cellular inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;
KW c-IAP-2; prophylaxis; infection; inflammation; tumor formation.
XX
OS Homo sapiens.
XX
PN US5958771-A.
XX
PD 28-SEP-1999.
XX
PF 03-DEC-1998; 98US-0205144.
XX
PR 03-DEC-1998; 98US-0205144.
XX
PA (ISIS-) ISIS PHARM INC.
PI Bennett CF, Coweart LM, Ackermann EJ;
XX
DR WPI: 1999-561046/47.
DR N-PSDB; AA222096.
XX
XX
PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2
PT useful for e.g. diagnostics, therapeutics, and as research reagents
XX
PS Example 13; Columns 45-50; 33pp; English.
XX
XX
CC The invention provides antisense compounds of 8-30 nucleotides that
CC inhibit the expression of human Cellular Inhibitor of Apoptosis-2
CC (c-IAP-2). The antisense compounds may be used for diagnostics,
CC therapeutics (for modulating the expression of c-IAP-2), prophylaxis
CC (e.g. to prevent or delay infection, inflammation, or tumor formation),
CC as research reagents (e.g. to distinguish between members of a biological
CC pathway) and in kits. The present sequence represents the human cellular
CC inhibitor of apoptosis-2.

XX
SQ Sequence 604 AA;

Query Match 100.0%; Score 267; DB 20; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.3e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACACGKLSNWEKDNAMSEHLRHPKCP 46
Db 189 LAKAGFYIIGPDRVACACGKLSNWEKDNAMSEHLRHPKCP 234

RESULT 6
AAU97837

ID AAU97837 standard; Protein; 1140 AA.
 XX
 AC AAU97837;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human cysteine protease fusion protein API2-MLT (CPG2).
 XX
 KW Cystiene protease; CPG2; cell-cell adhesion; lymphoma; osteoporosis;
 KW rheumatoid arthritis; inflammatory disease; irritable bowel disease;
 KW respiratory disease; asthma; autoimmune disease; bone disease;
 KW atherosclerosis; neoplastic disease; melanoma; prostate; lung tumour;
 KW ovary tumour; myeloproliferative disorder; leukaemia; metastasis;
 KW heart disease; myocardial infarction; cardiac failure; API2-MLT;
 KW reperfusion injury; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; neurological disorder; stroke; muscular dystrophy;
 KW liver disease; cataract; infection; transgenic animal; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200233058-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 22-OCT-2001; 2001WO-GB04698.
 XX
 PR 20-OCT-2000; 2000GB-0025816.
 PR 29-JAN-2001; 2001GB-0002260.
 XX
 PA (INPH-) INPHARMATICA LTD.
 XX
 PI Fagan RJ, Phelps CB, Gutteridge A, Nicholls RG;
 XX
 DR WPI; 2002-463311/49.
 DR N-PSDB; ABR52387.
 XX
 PT New proteins identified as cysteine proteases for diagnosing,
 PT preventing and treating neoplastic, inflammatory, autoimmune diseases
 PT and neurological disorders
 XX
 PS Claim 1; Fig 15; 129pp; English.
 XX
 CC This sequence represents a polypeptide (I) termed BAA83099.1 (CPG1),
 CC AAD46161.1 (CPG2) or AAD8507.2 (CPG3), identified as a cysteine
 CC protease, its fragment having cysteine protease activity or having an
 CC antigenic determinant in common with the polypeptide, or its functional
 CC equivalent. (I) is useful as a cysteine protease and for effecting
 CC cell-cell adhesion. A nucleic acid (II) encoding (I) is useful for
 CC expressing a protein that possesses cysteine protease activity. (I),
 CC (II), a vector (III) comprising (II), a ligand (IV) which binds (I) and
 CC a compound (V) that alters the activity of (I), are useful for treating
 CC diseases in which the expression of the natural gene or the activity of
 CC the polypeptide is higher or lower in a diseased patient when compared
 CC to the level of expression or activity in a healthy patient. (I) - (V)
 CC are useful in therapy or diagnosis of disease and in the manufacture of
 CC a medicament for treating lymphoma, rheumatoid arthritis, osteoporosis,
 CC inflammatory disease, such as irritable bowel disease, respiratory
 CC disease such as asthma, autoimmune disease, bone disease,
 CC atherosclerosis, neoplastic diseases, such as melanoma, prostate, lung
 CC and ovary tumours, myeloproliferative disorder, leukaemia, metastasis,
 CC heart disease, myocardial infarction, cardiac failure, reperfusion
 CC injury, neurodegenerative diseases such as Alzheimer's disease,
 CC Parkinson's disease, neurological disorder, stroke, muscular dystrophy,
 CC liver disease, cataract, infection such as bacterial, parasitic,
 CC Plasmodium and viral infection. A transgenic or knockout non-human animal
 CC is useful as an animal model to screen for a compound effective to treat
 CC a disease. This sequence encodes cysteine protease fusion protein
 CC API2-MLT (CPG2) described in the invention.
 XX
 SQ Sequence 1140 AA;
 Query Match 100.0%; Score 267; DB 23; Length 1140;
 Best Local Similarity 100.0%; Pred. No. 2.6e-25;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
 DB 189 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 234

RESULT 7

AAB50694
 ID AAB50694 standard; Protein; 1141 AA.

AC AAB50694;
 XX

DT 19-MAR-2001 (first entry)
 XX

DE Human API2-MLT chimeric protein sequence.
 XX

KW Human; API2-MLT chimera; chimeric; apoptosis inhibitor 2; MLT; API2;
 KW mucosa-associated lymphoid tissue lymphoma associated translocation;
 KW chromosome 11 region q21-22.3; chromosome 18 region q21.1-22;
 KW molecular characterisation; chromosome translocation; carcinogenesis;
 KW fusion protein; malignancy.
 KW
 XX

OS Chimeric - Homo sapiens.
 OS Synthetic.
 XX

PN WO200073500-A1.
 XX

PD 07-DEC-2000.
 XX

PF 26-MAY-2000; 2000WO-EP04796.
 XX

PR 27-MAY-1999; 99EP-0201683.
 XX

PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECNOG.
 XX

PI Baens M, Marynen P, Dierlaam J;
 XX

DR WPI; 2001-061556/07.
 DR N-PSDB; AAC90972.
 XX

PT Determining if a tissue sample has a chromosome (11:18) translocation
 PT associated with malignancies by amplifying a nucleic acid sample using
 PT primers complementary to chromosome 11 region q21-22.3 and chromosome
 PT 18 region q21.1-22
 XX

PS Claim 12; Fig 5; 47pp; English.
 XX

CC The present invention describes a method for determining if a tissue
 CC sample comprises a cell with a chromosome (11:18) translocation
 CC associated with malignancies such as mucosa-associated lymphoid tissue
 CC (MALT) lymphomas. The method comprises subjecting a sample nucleic acid
 CC to amplification using primers complementary to sequences which are on
 CC chromosome 11 region q21-22.3 and on chromosome 18 region q21.1-22. The
 CC method can be used for determining if a tissue sample or analogue
 CC comprises a chromosome (11:18) translocation associated with malignancies
 CC such as mucosa-associated lymphoid tissue lymphomas. The nucleic acid or
 CC the antibody may be used as a probe for detection, for hybridisation to
 CC southern blot cell DNA or for in situ hybridisation of cells, or for
 CC determining the presence of complementary DNA. The present sequence
 CC represents the specifically claimed chimeric human apoptosis inhibitor 2
 CC (API2)/MALT-lymphoma associated translocation (MLT) protein.
 XX

SQ Sequence 1141 AA;
 Query Match 100.0%; Score 267; DB 22; Length 1141;
 Best Local Similarity 100.0%; Pred. No. 2.6e-25;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 46
 DB 189 LAKAGFYIIGPDRVACFACGKLSNWEPKDNAMSEHLRHPKCP 234

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:51:32 ; Search time 1.90783 Seconds

(without alignments)
1000.040 Million cell updates/sec

Title: US-08-569-749-8

Sequence: 1 LAKAGFYITGPDGRVACRAC.....WEIKDNAMSEHLRHPKCPF 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	267	100.0	604	BIR2_HUMAN	Q13489 homo sapien
2	254	95.1	358	PIAP_PIG	Q62640 sus scrofa
3	248	92.9	618	BIR3_HUMAN	Q13490 homo sapien
4	247	92.5	612	BIR3_MOUSE	Q62210 mus musculu
5	235	88.0	600	BIR2_MOUSE	Q08863 mus musculu
6	186	69.7	611	BIR_CHICK	Q90660 gallus gall
7	182	68.2	497	BIR4_HUMAN	P98170 homo sapien
8	177	66.3	496	BIR4_MOUSE	Q60989 mus musculu
9	175	65.5	496	BIR4_RAT	Q9R016 rattus norv
10	145	54.3	236	BIR8_HUMAN	Q96P09 homo sapien
11	145	54.3	236	BIR8_PANTR	Q95M72 pan troglod
12	145	54.3	498	BIR8_MOUSE	Q24307 drosophila
13	144	53.9	236	BIR8_GORGO	Q95M71 gorilla gor
14	141	52.8	1402	BIR_MOUSE	Q9J1D3 mus musculu
15	141	52.8	1403	BIR1_HUMAN	Q13075 homo sapien
16	141	52.8	1403	BIR_MOUSE	Q9QW45 mus musculu
17	141	52.8	1403	BIR_MOUSE	Q9R016 mus musculu
18	141	52.8	1403	BIR_MOUSE	Q9J1D3 mus musculu
19	138	51.7	1447	BIR_MOUSE	Q9QW44 mus musculu
20	135	50.6	268	IAP3_NPYOP	P41437 oryza pseu
21	131	49.1	275	IAP_GVCP	P41437 oryza pseu
22	129	48.3	438	IAP1_DROME	Q24306 drosophila
23	122.5	45.9	4829	BIR6_HUMAN	Q9N109 homo sapien
24	121	45.3	298	BIR6_HUMAN	Q96C85 homo sapien
25	112	41.9	239	IRF6	P47732 chilo iride
26	105.5	39.5	140	BIR5_MOUSE	Q70201 mus musculu
27	105.5	39.5	142	BIR5_RAT	Q9J1H7 rattus norv
28	103	38.6	997	BIR1_SCHPO	Q14064 schizosacch
29	93	34.8	286	IAP1_NPYAC	P41435 autographa
30	92.5	34.6	142	BIR5_HUMAN	Q15392 homo sapien
31	90	33.7	275	IAP1_NPYOP	Q10296 oryza pseu
32	72.5	27.2	224	IAPL_ASRB7	Q65138 african swi
33	69.5	26.0	224	IAPL_ASRF1	Q11452 african swi

ALIGNMENTS

RESULT 1	ID	STANDARD	PRT	604 AA
BIR2_HUMAN	AC	Q13489; Q16628; Q9UP46; Q9HC27;		
BIR2_HUMAN	DT	01-NOV-1997 (Rel. 35, Created)		
BIR2_HUMAN	DT	01-NOV-1997 (Rel. 35, Last sequence update)		
BIR2_HUMAN	DT	15-JUN-2002 (Rel. 41, Last annotation update)		
BIR2_HUMAN	DE	Baculoviral IAP repeat-containing protein 1 (Inhibitor of apoptosis protein 1) (IAP1) (IAP-1) (C-IAP2) (TNFR2-TNFR signaling complex protein 1) (IAP homolog C).		
BIR2_HUMAN	GN	BIRC2 OR API1 OR IAP1 OR MHC.		
BIR2_HUMAN	OS	Homo sapiens (Human).		
BIR2_HUMAN	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
BIR2_HUMAN	OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
BIR2_HUMAN	OX	NCBI_TaxID=9606;		
BIR2_HUMAN	RN	[1]		
BIR2_HUMAN	RP	SEQUENCE FROM N.A.		
BIR2_HUMAN	RC	TISSUE=Liver;		
BIR2_HUMAN	RX	MEDLINE=96128127; PubMed=8548810;		
BIR2_HUMAN	RA	Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;		
BIR2_HUMAN	RT	"The TNFR2-TNFR signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";		
BIR2_HUMAN	RT	Cell 83:1243-1252(1995).		
BIR2_HUMAN	RN	[2]		
BIR2_HUMAN	RP	SEQUENCE FROM N.A.		
BIR2_HUMAN	RC	TISSUE=Liver;		
BIR2_HUMAN	RX	MEDLINE=96149249; PubMed=8552191;		
BIR2_HUMAN	RA	Liston P., Roy N., Tamai K., Lefebvre C., Balrd S., Cherton-Horvat G.,		
BIR2_HUMAN	RT	Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;		
BIR2_HUMAN	RT	"Suppression of apoptosis in mammalian cells by NAPI and a related family of IAP genes.";		
BIR2_HUMAN	RT	Nature 379:349-353(1996).		
BIR2_HUMAN	RN	[3]		
BIR2_HUMAN	RP	SEQUENCE FROM N.A.		
BIR2_HUMAN	RC	TISSUE=Fetal liver;		
BIR2_HUMAN	RX	MEDLINE=96209843; PubMed=8643514;		
BIR2_HUMAN	RA	Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;		
BIR2_HUMAN	RT	"Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";		
BIR2_HUMAN	RT	Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).		
BIR2_HUMAN	RN	[4]		
BIR2_HUMAN	RP	SEQUENCE FROM N.A.		
BIR2_HUMAN	RX	MEDLINE=99252096; PubMed=10233894;		
BIR2_HUMAN	RA	Horrevoets A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,		
BIR2_HUMAN	RT	ten Cate J.W., Pannekoek H.;		
BIR2_HUMAN	RT	"Vascular endothelial genes that are responsive to tumor necrosis factor-alpha in vitro are expressed in atherosclerotic lesions, including inhibitor of apoptosis protein-1, stannin, and two novel genes.";		
BIR2_HUMAN	RT	Blood 93:3418-3431(1999).		
BIR2_HUMAN	RN	[5]		
BIR2_HUMAN	RP	SEQUENCE OF 362-441 FROM N.A.		
BIR2_HUMAN	RX	MEDLINE=20519161; PubMed=11066071;		
BIR2_HUMAN	RA	Baens M., Steyels A., Dierlam J., De Wolf-Peters C., Marynen P.;		
BIR2_HUMAN	RT	"Structure of the MTR gene and molecular characterization of the genomic breakpoint junctions in the t(11;18)(q21;q21) of marginal zone		

34	66.5	24.9	224	1	IAPL_ASRF3	Q11451 african swi
35	66.5	24.9	224	1	IAPL_ASRF3	Q12407 african swi
36	66.5	24.9	238	1	IAPL_ASRF2	Q11453 african swi
37	60	22.5	249	1	IAP2_NPYAC	P41454 autographa
38	59.5	22.3	404	1	FPR1_METTM	Q50497 methanobact
39	57.5	21.5	278	1	HUP1_RHOCA	Q03009 rhodobacter
40	56.5	21.2	706	1	SM2A_DROME	Q24323 drosophila
41	56.5	21.2	2236	1	PYR1_DROME	P05990 drosophila
42	56	21.0	1004	1	AT1B_ARPSF	P28774 artemia san
43	55	20.6	1433	1	CAT8_YEAST	P39113 saccharomyc
44	54	20.2	181	1	VG79_HSV11	Q00148 ictaluriid h
45	54	20.2	606	1	WDRL_HUMAN	Q75083 homo sapien

```

RT B-cell lymphomas of MALT type."
RL Genes Chromosomes Cancer 29:281-291(2000).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation
CC recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid
CC tissue). This translocation is found in approximately 50% of
CC cytogenetically abnormal low-grade MALT lymphoma and involves
CC MALT1 and BIRC2.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: LA9432; AAC41943.1; -
DR EMBL: U45878; AAC50371.1; -
DR EMBL: U37546; AAC50507.1; -
DR EMBL: AF070674; AAC83232.1; -
DR EMBL: AF178945; AAC09369.1; -
DR HSSP: Q13490; 1QBH.
DR Genew: HGNC:591; BIRC3.
DR MIM: 601712; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; Chromosomal translocation.
FT REPEAT 29 96 BIR 1.
FT REPEAT 169 235 BIR 2.
FT REPEAT 255 322 BIR 3.
FT DOMAIN 439 529 CARD.
FT ZN_FING 557 592 CARD.
FT SITE 442 443 RING-TYPE.
FT CONFLICT 18 18 N->Y (IN REF. 4).
FT CONFLICT 119 119 N->H (IN REF. 2).
FT CONFLICT 153 153 D->E (IN REF. 2).
FT CONFLICT 163 163 H->P (IN REF. 2).
FT CONFLICT 165 165 A->P (IN REF. 2).
FT CONFLICT 191 191 K->R (IN REF. 2).
FT CONFLICT 364 364 F->L (IN REF. 2).
FT CONFLICT 552 552 Q->P (IN REF. 2).
SQ SEQUENCE 604 AA; 68371 MW; 8581A00BA9AAB4A7 CRC64;

Query Match 100.0%; Score 267; DB 1; Length 604;
Best local similarity 100.0%; Pred. No. 5.7e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LAKAGFYIIGPGRVACFACGKLSNWPCKDNAMSEHLRHPKCP 46
DB 189 LAKAGFYIIGPGRVACFACGKLSNWPCKDNAMSEHLRHPKCP 234

RESULT 2
ID PIAP_PIG STANDARD; PRT; 358 AA.
AC 062640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative inhibitor of apoptosis.
GN PIAP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBL:Taxid-9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Aorta;
RX MEDLINE:98162622; PubMed-9501011;
RA Stehlik C., de Martin R., Binder B.R., Liipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
RT protein (Iap) family member is regulated by NF-kappa B.";
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U79142; AAC39171.1; -
DR HSSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT DOMAIN 193 283 CARD.
FT ZN_FING 311 346 RING-TYPE.
SQ SEQUENCE 358 AA; 40977 MW; EB2268BA9A6190A4 CRC64;

Query Match 95.1%; Score 254; DB 1; Length 358;
Best local similarity 93.5%; Pred. No. 1.6e-25;
Matches 43; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 LAKAGFYIIGPGRVACFACGKLSNWPCKDNAMSEHLRHPKCP 46
DB 24 LAKAGFYIIGPGRVACFACGKLSNWPCKDNAMTEHLRHPKCP 69

RESULT 3

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BIR3_HUMAN
ID BIR3_HUMAN STANDARD: PRT: 618 AA.
AC 013490; 016516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis protein 2) (IAP2) (HIAF-2) (C-IAP1) (TNFR2-TRAF signaling complex)
DE BIR3 OR API2 OR IAP2 OR MIH2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liston P., Roy N., Tamal K., Lefebvre C., Baird S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Fetal liver;
RA MEDLINE=96209843; PubMed=8643514;
RT Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
RN [5]
RP STRUCTURE BY NMR OF 266-363.
RX MEDLINE=99332054; PubMed=10404221;
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat.";
RL Nat. Struct. Biol. 6:648-651(1999).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES. MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY, AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infoblogn.fr/services/chromocancer/Genes/BIR3ID239.html".
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CC CC
DR EMBL: L49431; AAC41942.1;
DR EMBL: U45879; AAC50372.1;
DR EMBL: U37547; AAC50508.1;
DR EMBL: BC016174; AAH16174.1;
DR PDB: 1OBH; 20-OCT-99.
DR Genew; HGNC:590; BIRC2.
DR MIM: 601721;
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR KW Apoptosis; Zinc-finger; Repeat; 3D-structure.
FT REPEAT 46 113 BIR 1.
FT REPEAT 184 250 BIR 2.
FT REPEAT 269 336 BIR 3.
FT DOMAIN 453 543 CARD.
FT ZN_FING 571 606 CARD-TYPE.
FT CONFLICT 157 157 S -> P (IN REF. 2).
FT CONFLICT 308 308 C -> G (IN REF. 2).
FT CONFLICT 414 414 Q -> L (IN REF. 2).
FT CONFLICT 514 514 L -> W (IN REF. 2).
SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 92.9%; Score 248; DB 1; Length 618;
Best local Similarity 91.3%; Pred. No. 1,7e-24;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIISPGDRVACFACGKLSNWEKDNSEHLRHPKCP 46
DB 204 LAKAGFYIISPGDRVACFACGKLSNWEKDNSEHLRHPKCP 249

RESULT 4
BIR3_MOUSE STANDARD: PRT: 612 AA.
ID BIR3_MOUSE
AC 062210; 008864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (inhibitor of apoptosis protein 2) (MIAP2) (MIAP-2).
GN BIR3 OR API2 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RA Liston P., Lefebvre C., Pong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein

```
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: L49433; AAC42078.1; -.
DR EMBL: U88909; AAC53532.1; -.
DR HSSP: Q13490; 1QBH.
DR MGD: MGI:1197009; Birc3.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
DR REPEAT 46 113 BIR 1.
DR REPEAT 177 243 BIR 2.
DR REPEAT 262 329 BIR 3.
DR DOMAIN 447 537 CARD.
DR ZN_RING 565 600 CARD.
DR CONFLICT 380 380 E -> K (IN REF. 2).
DR SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 92.5%; Score 247; DB 1; Length 612;
Best Local Similarity 91.3%; Pred. No. 2.2e-24;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LAKAGFYIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 197 LAKAGFYIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 242

RESULT 5
BIR2_MOUSE STANDARD; PRT; 600 AA.
AC 008863;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 1) (MIAP1) (MIAP-1).
GN BIRC2 OR API1 OR IAP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U88908; AAC53531.1; -.
DR HSSP: Q13490; 1QBH.
DR MGD: MGI:1197007; Birc2.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
DR REPEAT 27 94 BIR 1.
DR REPEAT 167 233 BIR 2.
DR REPEAT 253 320 BIR 3.
DR DOMAIN 436 525 CARD.
DR ZN_RING 553 588 RING-TYPE.
DR SEQUENCE 600 AA; 67198 MW; AD7F73E6849317D1 CRC64;

Query Match 88.0%; Score 235; DB 1; Length 600;
Best Local Similarity 89.1%; Pred. No. 7.7e-23;
Matches 41; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 LAKAGFYIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
Db 187 LAKAGFYIGPDRVACFACGKLSNWEKDNAMSEHLRHPKCP 232

RESULT 6
BIR_CHICK STANDARD; PRT; 611 AA.
AC Q90660;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (Inhibitor of T cell apoptosis
DE protein).
GN ITA.
```

OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=97101112; PubMed=8945639;
 RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;
 RT "ITA, a vertebrate homologue of IAP that is expressed in T
 lymphocytes.";
 RL DNA Cell Biol. 15:981-988(1996).
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
 CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
 CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
 CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
 CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC -----
 CC DR EMBL: U27466; AAB48118.1; -.
 DR HSSB: Q13490; IOBH.
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 3.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Apoptosis; Zinc-finger; Repeat; Nuclear protein.
 FT REPEAT 30 97 BIR 1.
 FT REPEAT 176 242 BIR 2.
 FT REPEAT 262 329 BIR 3.
 FT DOMAIN 446 536 CARD.
 FT ZN_FING 564 599 RING-TYPE.
 SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;
 Query Match 69.7%; Score 186; DB 1; Length 611;
 Best Local Similarity 71.7%; Pred. No. 1.7e-16;
 Matches 33; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 QY 1 LAKAGFYIIGPDRAVACGKLSNWEPRKDNAMSEHLRHFECPE 46
 DB 196 VAKAGLDDLTADKAVACVNCVKLSNWEPRKDNAMSEHRRHFPNCP 241
 RESULT 7
 BIR4_HUMAN
 ID BIR4_HUMAN STANDARD; PRT; 497 AA.
 AC P98170; Q9NQ14;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis

DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
 DE (IAP-like protein) (HILP).
 GN BIR4 OR API3 OR IAP3 OR XIAP.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=96149249; PubMed=8552191;
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertov-Horvat G.,
 RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korbelux R.G.;
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related
 RT family of IAP genes.";
 RL Nature 379:349-353(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal heart;
 RX MEDLINE=96256286; PubMed=8654366;
 RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
 RA Gillilan M.C., Shieles H., Hardwick J.M., Thompson C.B.;
 RT "A conserved family of cellular genes related to the baculovirus iap
 RT gene and encoding apoptosis inhibitors.";
 RL EMBO J. 15:2685-2694(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Grahnam D.;
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=97373959; PubMed=9230442;
 RA Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;
 RT "X-linked IAP is a direct inhibitor of cell-death proteases.";
 RL Nature 388:300-304(1997).
 RN [5]
 RP MUTAGENESIS OF ASP-148; ASP-214; ASN-259; TRP-310 AND GLU-314.
 RX MEDLINE=21634829; PubMed=11604410;
 RA Verhagen A.M., Silke J., Ewert P.G., Pakusch M., Kaufmann H.,
 RA Connolly L.M., Day C.L., Tikoo A., Burke R., Wrobel C., Moritz R.L.,
 RA Simpson R.J., Vaux D.L.;
 RT "HtrA2 promotes cell death through its serine protease activity and
 RT its ability to antagonize inhibitor of apoptosis proteins.";
 RL J. Biol. Chem. 277:445-454(2002).
 RN [6]
 RP STRUCTURE BY NMR OF 241-356 IN COMPLEX WITH SMAC.
 RX MEDLINE=21020961; PubMed=11140637;
 RA Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T.,
 RA Hermann J., Wu J.C., Fesik S.W.;
 RT "Structural basis for binding of Smac/Diablo to the XIAP BIR3
 RT domain.";
 RL Nature 408:1004-1008(2000).
 CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9.
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
 CC inhibit apoptotic suppressor activity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: UBQUITOUS, EXCEPT PERIPHERAL BLOOD
 CC LEUKOCYTES.
 CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
 CC and -7, while the third BIR is involved in caspase-9 inhibition.
 CC The interactions with SMAC and PRSS25 are mediated by the second
 CC and third BIR domains.
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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CC -----
DR EMBL; U45880; AAC50373.1; -.
DR EMBL; U32974; AAC50518.1; -.
DR EMBL; AL121601; CAB95312.1; -.
DR PDB; 1G3F; 10-JAN-01.
DR Genew; HGNC:592; BIRC4.
DR MIM; 300079; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_r1ng.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS500518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor;
KW 3D-structure.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 265 330 BIR 3.
FT ZN_FING 450 485 RING-TYPE.
FT ZN_FING 214 214 D->S: REDUCED INTERACTION WITH PRSS25.
FT MUTAGEN 314 314 E->S: DECREASED INTERACTION WITH SMAC AND
FT WITH PRSS25.
FT CONFLICT 162 162 S -> C (IN REF. 1).
FT CONFLICT 423 423 Q -> P (IN REF. 2).
SQ SEQUENCE 497 AA; 56684 MW; 9D394C16D45EB635 CRC64;

Query Match 68.2%; Score 182; DB 1; Length 497;
Best Local Similarity 69.6%; Pred. No. 4.5e-16;
Matches 32; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

OY 1 LAKAGFYIGPDYVACFACGKLSNWEPRDNAMSEHLRHPKCP 46
DB 184 LASAGLYTGTGDDVOVCFCCGKLNWEPDRAMSEHRHFPNCF 229

RESULT 8
BIR4_MOUSE STANDARD; PRT; 496 AA.
ID BIR4_MOUSE
AC Q60989; O08865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN BIRC4 OR API3 OR XIAP OR ALPA OR MIHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; Pubmed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (By similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
```

```
CC -----
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRSS25 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U36842; AAC52594.1; -.
DR EMBL; U88990; AAB58376.1; -.
DR HSSP; Q13490; IOBH.
DR MGD; MGI:107572; Birc4.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_r1ng.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS500518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
FT CONFLICT 208 208 E -> K (IN REF. 2).
FT CONFLICT 317 317 E -> D (IN REF. 2).
FT CONFLICT 322 322 W -> C (IN REF. 2).
FT CONFLICT 346 346 S -> P (IN REF. 2).
FT CONFLICT 360 360 S -> P (IN REF. 2).
FT CONFLICT 388 388 I -> L (IN REF. 2).
FT CONFLICT 449 449 C -> S (IN REF. 2).
FT CONFLICT 462 462 V -> F (IN REF. 2).
FT CONFLICT 468 468 V -> A (IN REF. 2).
FT CONFLICT 490 490 K -> N (IN REF. 2).
SQ SEQUENCE 496 AA; 56079 MW; EC5FEA0799F2CDD8 CRC64;

Query Match 66.3%; Score 177; DB 1; Length 496;
Best Local Similarity 67.4%; Pred. No. 2e-15;
Matches 31; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

OY 1 LAKAGFYIGPDYVACFACGKLSNWEPRDNAMSEHLRHPKCP 46
DB 184 LASAGLYTGTGDDVOVCFCCGKLNWEPDRAMSEHRHFPNCF 229

RESULT 9
BIR4_RAT STANDARD; PRT; 496 AA.
ID BIR4_RAT
AC Q9R016;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (RIAP3) (RIAP-3).
GN BIRC4 OR API3 OR XIAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Saito N.;
```


RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT Apoptosis protein family."
RL Mol. Cell. Biol. 21:4292-4301(2001).
CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SUBUNIT: Binds to caspase-9 (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: AY030052; AAK49776.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR, 1.
DR Pfam: PF00097; Zf-C3HC4, 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS00089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger.
FM REPEAT 7 70 BIR.
FM ZN_FING 189 224 RING-TYPE.
SQ SEQUENCE 236 AA: 27136 MW: 640CA3A251420EDE CRC64;
Query Match 54.3%; Score 145; DB 1; Length 236;
Best Local Similarity 50.0%; Pred. No. 1.3e-11;
Matches 23; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
OY 1 LAKAGFYIIGPDRAVACGKLSWEPKDNAMSEHLRHPKPF 46
Db 23 IARAGFYAIGEDKVCFCGCGGLANWKPRDPDQAHAKWPGCKY 68
RESULT 12
IAP2_DROME STANDARD; PRT; 498 AA.
AC Q24307; Q24177; Q24115; Q24149; Q9V7G1;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis 2 inhibitor (inhibitor of apoptosis 2) (DIAP2) (DIAP) (IAP
DE homolog A) (IAP-like protein) (DILP).
GN IAP2 OR ILP OR DIHA OR CG8293.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye Imaginal disk;
RX MEDLINE=96128128; PubMed=8548811;
RA Hay B.A., Wassarman D.A., Rubin G.M.;
RT "Drosophila homolog of baculovirus inhibitor of apoptosis proteins
RT function to block cell death."
RL Cell 83:1253-1262(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=96149249; PubMed=8552191;
RA Iatton P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";

RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=96256286; PubMed=8654366;
RA Duckett C.S., Naya V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
RA Gilliland M.C., Shies H., Hardwick J.M., Thompson C.B.;
RT "A conserved family of cellular genes related to the baculovirus iap
RT gene and encoding apoptosis inhibitors."
RL EMBO J. 15:2685-2694(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RA Ross J.L.;
RL Thesis (1991), Vanderbilt University / Nashville, U.S.A.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibgwam C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylvestre R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [6]
RP SEQUENCE OF 17-498 FROM N.A.
RC TISSUE=Larva;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [7]
RP SEQUENCE FROM N.A.
RC HID-DEPENDENT CELL DEATH IN THE EYE.
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND
CC DEVELOPMENT.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS THROUGHOUT
CC DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC
CC EMBL; L49441; AAC41610.1; -
CC EMBL; U45881; AAC46988.1; -
CC EMBL; U32373; AAC47155.1; -
CC EMBL; M96581; -; NOT_ANNOTATED_CDS.
CC EMBL; AE003809; AAF58095.1; -
CC EMBL; U38809; AAB08398.1; -
CC HSP; Q13490; IOBH.
CC FlyBase; FBgn0015247; Iap2.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR001841; Zn_fing.
CC Pfam; PF00097; zf-C3HC4; 1.
CC SMART; SM0053; BIR; 3.
CC SMART; SM00238; BIR; 3.
CC SMART; SM00184; RING; 1.
CC PROSITE; PS01282; BIR_REPEAT_1; 3.
CC PROSITE; PS50143; BIR_REPEAT_2; 3.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS50089; ZF_RING_2; 1.
CC Apoptosis; Zinc_finger; Repeat.
CC REPEAT 9 76 BIR 1.
CC REPEAT 113 179 BIR 2.
CC REPEAT 212 279 BIR 3.
CC ZN_FING 451 486 RING-TYPE.
CC CONFLICT 5 5 G -> V (IN REF. 2).
CC CONFLICT 40 40 N -> K (IN REF. 2).
CC CONFLICT 64 65 ER -> AG (IN REF. 3).
CC CONFLICT 94 94 E -> K (IN REF. 1).
CC CONFLICT 282 282 A -> D (IN REF. 6).
CC CONFLICT 286 286 A -> S (IN REF. 3).
CC CONFLICT 302 302 P -> Q (IN REF. 2 AND 5).
CC CONFLICT 303 303 P -> T (IN REF. 6).
CC CONFLICT 327 327 A -> T (IN REF. 2).
CC SEQUENCE 369 376 ALEVERPP -> DWRCASR (IN REF. 3).
CC 498 AA; 54506 MW; 66EC36DA6ED24AD6 CRC64;
CC
CC Query Match 54.3%; Score 145; DB 1; Length 498;
CC Best Local Similarity 55.6%; Pred. No. 2.8e-11;
CC Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;
CC
CC Oy 1 LAKAGFYIIGPDRAVACFACGKLSNWEPKDNAMSEHLRHFPCP 45
CC |||||: | | | | : | | | | | | | |
CC Db 133 LAKAGFYILRLDHWKCVCWNGYIAKWEKNDNAFEEHRRFFQCP 177
CC
CC RESULT 13
CC BIR8_GORGO
CC ID BIR8_GORGO STANDARD; PRT; 236 AA.
CC AC 095M71;
CC DT 15-JUN-2002 (Rel. 41, Created)
CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
CC like protein 2) (IAP-like protein 2) (ILP-2).
CC GN BIRC8 OR ILP2.
CC OS Gorilla gorilla gorilla (Lowland gorilla).
CC CC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
CC CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Gorilla.
CC CC NCBI_taxid=9595;
CC OX [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=21286921; PubMed=11390657;
CC RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
CC Fratini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
CC Notarangelo L.D., Vezoni P., Fearhnd H.O., Duckett C.S.;

```

```
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of  
RT apoptosis protein family."  
RL Mol. Cell. Biol. 21:4292-4301(2001).  
CC -I FUNCTION: Protects against apoptosis mediated by BAX (By  
CC similarity).  
CC -I SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -I SUBUNIT: Binds to caspase-9 (By similarity).  
CC -I SIMILARITY: BELONGS TO THE IAP FAMILY.  
CC -I SIMILARITY: CONTAINS 1 BIR REPEAT.  
CC -I SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
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-----  
DR EMBL; AY030053; AAK49777.1; -.  
DR InterPro; IPRO01370; BIR.  
DR InterPro; IPRO01841; Zn_fing.  
DR Pfam; PF00653; BIR; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR PROSITE; PS01282; BIR_REPEAT_1; FALSE_NEG.  
DR PROSITE; PS50143; BIR_REPEAT_2; 1.  
DR PROSITE; PS00518; zf_RING_1; FALSE_NEG.  
DR PROSITE; PS50089; zf_RING_2; 1.  
DR Apoptosis; Zinc-finger.  
FT REPEAT 7 70 BIR.  
FT ZN_FING 189 224 RING-TYPE.  
SQ SEQUENCE 236 AA; 27120 MW; C3A70E39EE442E4C CRC64;  
  
Query Match 53.9%; Score 144; DB 1; Length 236;  
Best Local Similarity 47.8%; Pred. No. 1.8e-11;  
Matches 22; Conservative 11; Mismatches 13; Indels 0; Gaps 0;  
  
QY 1 LAKAGFYIYGPDRAVACFACGSKLSNWEPKDNAMSEHLRHFPKCP 46  
Db 23 LARAGFAITGEDDKIQCFHCGGLANWKPKEDPWEOHAkWYFGCKY 68  
||:||||| || |::||| ||:||||: : |:| ||:  
RESULT 14  
BIR_MOUSE STANDARD; PRT; 1402 AA.  
ID ID BIR_MOUSE  
AC Q9JIB3:  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Baculoviral iAP repeat-containing protein Ig (Neuronal apoptosis  
DE inhibitory protein 7).  
GN BIRCIG OR NAIP7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OCC Mamalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20414747; PubMed=10958627;  
RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;  
RT "Genomic sequence analysis of the mouse Naip gene array.";  
RL Genome Res. 10:1095-1102(2000).  
CC -I FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -I SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -I SIMILARITY: CONTAINS 1 NACHT DOMAIN.  
-----  
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CC -----
DR EMBL; AF242433; AAF82749.1; -.
DR HSSP; Q13490; IQBH.
DR MGD; MGI:1858256; Birc1g.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
DR Apoptosis; Repeat; Multigene family.
KW REPEAT
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1402 AA; 159662 MW; CIDFFBA359893E0D CRC64;

Query Match 52.8%; Score 141; DB 1; Length 1402;
Best Local Similarity 52.2%; Pred. No. 2.6e-10;
Matches 24; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

OY 1 LAKAGFYIYIGPDRVACFACGKLSNWEPRDNAMSEHLRHPKCP 46
DB 181 LSAAGFYTGKRDYQCFSCGSGSLGNWEGDDPWEKHAKEFPKCEF 226

RESULT 15
BIR1_HUMAN
ID BIR1_HUMAN STANDARD; PRT; 1403 AA.
AC 013075; Q13730; Q99796; O75857;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (neuronal apoptosis
DE inhibitory protein).
GN BIR1 OR NAIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Fetal brain;
RX MEDLINE=95112344; PubMed=7813013;
RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Varaghi Z.,
RA Farahani R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,
RA Salih M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O.,
RA de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;
RT "The gene for neuronal apoptosis inhibitory protein is partially
RT deleted in individuals with spinal muscular atrophy.";
RL Cell 80:167-178(1995).
RN [2]
RP SEQUENCE FROM N.A. AND REVISIONS.
RC TISSUE-Brain;
RX MEDLINE=98163755; PubMed=9503025;
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,
RA Xuan Q.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,
RA Mackenzie A.E.;
RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular
RT atrophy candidate genes SMN and NAIP.";
RL Genomics 48:121-127(1998).
RN [3]
RP SEQUENCE OF 386-623 FROM N.A.
RA der Steege G., Draalers T.G., Grootscholten P.M., Olinga J.,
RA Anzevin R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,
RA Buys C.H.C.M.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 222-1403 FROM N.A.
RA Jones K., Graves T., McPherson J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]

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RP FUNCTION.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.";
RL Nature 379:349-353(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY
CC NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN
CC SPINAL CORD.
CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN
CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE I). SMAS
CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I
CC (WERNIG-HOEFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE
CC III (WOLFF-PARK-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF
CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE
CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO
CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
CC NEWBORNS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL; U19251; AAC52045.1; -.
DR EMBL; U80017; AAC52047.1; -.
DR EMBL; U21913; AAA64504.1; -.
DR EMBL; AC005031; AAC62261.1; -.
DR HSSP; Q13490; IQBH.
DR Genew; HGNC:7634; BIR1.
DR MIM; 600355; -.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
KW Apoptosis; Repeat.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 758 NACHT.
FT CONFLICT 222 223 PK -> YR (IN REF. 4).
FT CONFLICT 386 387 VP -> ST (IN REF. 3).
FT CONFLICT 535 535 M -> V (IN REF. 3).
FT CONFLICT 553 553 Y -> H (IN REF. 3).
FT CONFLICT 1228 1231 MISSING (IN REF. 4).
SQ SEQUENCE 1403 AA; 159613 MW; 566304C154DA5E64 CRC64;

Query Match 52.8%; Score 141; DB 1; Length 1403;
Best Local Similarity 52.2%; Pred. No. 2.6e-10;
Matches 24; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

OY 1 LAKAGFYIYIGPDRVACFACGKLSNWEPRDNAMSEHLRHPKCP 46
DB 299 LAKAGFYTGKRDYQCFSCGSGSLGNWEGDDPWEKHAKEFPKCEF 344

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Search completed: May 5, 2003, 16:02:46
Job time : 2.90783 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:58:42 ; Search time 5.03456 Seconds

(Without alignments)
878.365 Million cell updates/sec

Title: US-08-569-749-8

Perfect score: 267
Sequence: 1 LAKAGFYIIGPDGVACFCAC.....MEPKDNAMSEHLRHPKCPF 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	264	98.9	604	2	apoptosis inhibitor
2	254	95.1	358	2	apoptosis inhibitor
3	248	92.9	618	2	apoptosis inhibitor
4	182	68.2	497	2	apoptosis inhibitor
5	145	54.3	496	2	apoptosis inhibitor
6	145	54.3	497	2	apoptosis inhibitor
7	141	52.8	1232	2	neutonal apoptosis
8	138	51.7	1447	2	neutonal apoptosis
9	135	50.6	268	2	inhibitor of apopt
10	135	50.6	268	2	inhibitor of apopt
11	131	49.1	275	2	apoptosis-inhibiti
12	122.5	45.9	4845	2	inhibitor-of-apopt
13	121	45.3	298	2	BIR repeat contain
14	112	41.9	208	2	kidney inhibitor o
15	103	38.6	997	2	probable apoptosis
16	100	37.5	150	2	cutl7 protein - fi
17	98	36.7	155	2	ORF MSV248 probabl
18	95	35.6	292	2	apoptosis inhibito
19	93	34.8	286	2	IAP1 orif27 - Bomby
20	90	33.7	275	2	apoptosis-inhibiti
21	74.5	27.9	329	2	ORF MSV242 probabl
22	68	25.5	155	2	apoptosis inhibito
23	62.5	23.4	223	2	hypothetical prote
24	60	22.5	249	2	apoptosis inhibito
25	60	22.5	249	2	IAP2 orif71 - Bomby
26	59	22.1	355	2	conserved hypothet
27	58	21.7	355	2	hypothetical prote
28	58	21.7	355	2	probable apoptosis
29	57.5	21.5	278	1	hupr protein - Rho

30	56.5	21.2	724	2	C49423	semaphorin II prec
31	56.5	21.2	2336	1	Q2FE	rudimentary protei
32	56	21.0	1004	2	JH0470	Na+/K+-exchanging
33	55	20.6	313	2	T02534	hypothetical prote
34	55	20.6	462	2	T47287	hypothetical prote
35	55	20.6	469	2	AB0237	probable membrane
36	55	20.6	469	2	T47015	hypothetical prote
37	55	20.6	1433	2	S54587	CAR8 protein - yea
38	54.5	20.4	546	2	AB1807	fumurate hydratase
39	54	20.2	181	2	E36794	hypothetical prote
40	54	20.2	606	2	T13152	WDRI protein - hum
41	54	20.2	843	1	A27340	complement C7 prec
42	53.5	20.0	172	2	T34035	hypothetical prote
43	53.5	20.0	563	1	VCWV7	env polypeptide -
44	53.5	20.0	741	2	T40095	zinc finger, C3HC4
45	53	19.9	838	2	A48440	ring-infected eryt

ALIGNMENTS

RESULT 1
S68449
apoptosis inhibitor hlap-1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68449
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraha
Nature 379, 349-353, 1996
A>Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68449
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: EMBL:U45878; NID:g1184315; PIDN:ANC50371.1; PID:g1184316
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:553-597/Domain: RING finger homology <RNG>

Query Match 98.9%; Score 264; DB 2; Length 604;
Best Local Similarity 97.8%; Pred. No. 1.1e-24;
Matches 45; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 LAKAGFYIIGPDGVACFCACGKLSNWEPRDNAMSEHLRHPKCPF 46
Db 189 LAKAGFYIIGPDGVACFCACGKLSNWEPRDNAMSEHLRHPKCPF 234

RESULT 2
JC5964
apoptosis inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Sep-2000
C:Accession: JC5964
R:Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A>Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap)
A:Reference number: JC5964; MUID:98162622; PMID:9501011
A:Accession: JC5964
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE>
A:Cross-references: GB:U79142; NID:g2957174; PIDN:ANC39171.1; PID:g2957175
C:Superfamily: RING finger homology
F:307-351/Domain: RING finger homology <RRN>

Query Match 95.1%; Score 254; DB 2; Length 358;
Best Local Similarity 93.5%; Pred. No. 1.2e-23;
Matches 43; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 46
|||||
Db 24 LAKAGFYIIGPDRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 69

RESULT 3

568450
apoptosis inhibitor hlap-2 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68450
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <LIS>
A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:567-611/Domain: RING finger homology <RNG>

Query Match

Best Local Similarity 92.9%; Score 248; DB 2; Length 618;
Matches 42; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 46
|||||
Db 204 LAKAGFYIIGPDRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 249

RESULT 4

569544
apoptosis inhibitor IAP homolog - human
C:Species: Homo sapiens (man)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S69544; S68451
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C. EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and en
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69544
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: EMBL:U32974; NID:g1016687; PIDN:AAC50518.1; PID:g1016688
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68451
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>
A:Cross-references: EMBL:U45880; NID:g1184319; PIDN:AAC50373.1; PID:g1184320
C:Genetics:
A:Gene: ilp
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

Query Match 68.2%; Score 182; DB 2; Length 497;
Best Local Similarity 69.6%; Pred. No. 1.2e-14;
Matches 32; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 46
|||||

Db 184 LASAGLYTIGIDYQCFCCGKLSNWEPRDNAMSEHLRHFPCPF 229

RESULT 5

568452
apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Nov-2000
C:Accession: S68452; S78528
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68452
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-496 <LIS>
A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
R:Baird, S.D.
Submitted to the EMBL Data Library, January 1996
A:Reference number: S78528
A:Accession: S78528
A:Molecule type: mRNA
A:Residues: 1-36, 'AT', 37, 'K', 39, 'L', 41-44, 'H', 46-58, 'Q', 60-412, 'A', 414-427, 'A', 429-49
A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
C:Genetics:
A:Cross-references: FlyBase:FBgn0015247
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:445-489/Domain: RING finger homology <RNG>

Query Match 54.3%; Score 145; DB 2; Length 496;
Best Local Similarity 55.6%; Pred. No. 4.2e-10;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 45
|||||
Db 131 LAKAGFYIIGPDRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 175

RESULT 6

569545
apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69545
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69545
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:Cross-references: EMBL:U32373; NID:g1019116; PIDN:AAC47155.1; PID:g1019117
C:Genetics:
A:Gene: ilp
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

Query Match 54.3%; Score 145; DB 2; Length 497;
Best Local Similarity 55.6%; Pred. No. 4.2e-10;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 45
|||||
Db 133 LAKAGFYIIGPDRVACFACGKLSNWEPRDNAMSEHLRHFPCPF 177

RESULT 7

A55478

```

A:Molecule type: DNA
A:Residues: 1-268 <AHR>
A:Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59034.1; VID:g1911281
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

Query Match          50.6%; Score 135; DB 2; Length 268;
Best Local Similarity 45.7%; Pred. No. 4e-09;
Matches 21; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGGKLSNWEPRKDNAMSEHLRHPKCP 46
||:||||:| | | | | | | | | | | | | | | | | | | | | |
DB 132 LAEGFFYTGQDKTRCFCCDGLKDWEPPDAPMOQHARWYDRCEY 177

RESULT 10
A53989
apoptosis-inhibiting protein - Oryza pseudotsugata multicapsid nuclear polyhedrosis
C:Species: Oryza pseudotsugata multicapsid nuclear polyhedrosis virus, OpNPV
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000
C:Accession: A53989
R.Birnbaum, M.J.; Clem, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a po
A:Reference number: A53989; MUID:94187094; PMID:8139034
A:Accession: A53989
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <BIR>
A:Cross-references: GB:L22564; NID:g456111; PIDN:AAB02610.1; PID:g456114
A:Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

Query Match          50.6%; Score 135; DB 2; Length 268;
Best Local Similarity 45.7%; Pred. No. 4e-09;
Matches 21; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGGKLSNWEPRKDNAMSEHLRHPKCP 46
||:||||:| | | | | | | | | | | | | | | | | | | | | |
DB 132 LAEGFFYTGQDKTRCFCCDGLKDWEPPDAPMOQHARWYDRCEY 177

RESULT 11
A45679
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis-virus Cpgv
C:Species: Cydia pomonella granulosis virus Cpgv
C:Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000
C:Accession: A45679
R.Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A:Reference number: A45679; MUID:93188168; PMID:8445726
A:Accession: A45679
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <CRO>
A:Cross-references: GB:L05494; NID:g289583; PIDN:AAA43935.1; PID:g289584
A:Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBI:P127015)
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match          49.1%; Score 131; DB 2; Length 275;
Best Local Similarity 45.7%; Pred. No. 1.3e-08;
Matches 21; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGGKLSNWEPRKDNAMSEHLRHPKCP 46
:||:|:| | | | | | | | | | | | | | | | | | | | | |
DB 129 MADAGFYTYGDMTKCFYCDGLKDWEPPDVPEQHVRWFDRCAV 174

RESULT 12
T31067
IIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse

```

C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T31067
R:Hauser, H.P.; Bardroff, M.; Pyrowolakis, G.; Jentsch, S.
J. Cell Biol. 141, 1415-1422, 1998
A:Title: A giant ubiquitin-conjugating enzyme related to IAP apoptosis inhibitors.
A:Reference number: Z20963; MID:98292517; PMID:9628897
A:Accession: T31067
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4845 <HAU>
A:Cross-references: EMBL:Y17267; NID:93319989; PID:CAA76720.1; PID:93319990
A:Note: localized to the Golgi compartment and the vesicular system
C:Keywords: membrane-associated protein

Query Match 45.9%; Score 122.5; DB 2; Length 4845;
Best Local Similarity 49.0%; Pred. No. 2.1e-06;
Matches 24; Conservative 3; Mismatches 19; Indels 3; Gaps 1;

OY 1 LAKAGFY--IGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46
DB 284 MAAGFYHQPASSGDDRAMCFCTSCVLCVMEPTDEPWEHERSPNCP 332

RESULT 13

JC7568
Kidney inhibitor of apoptosis protein - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7568
R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
Biochem. Biophys. Res. Commun. 279, 820-831, 2000
A:Title: KIAA, a novel member of the inhibitor of apoptosis protein family.
A:Reference number: JC7568; MID: 21092523; PMID:11162435
A:Contents: Fetal kidney
A:Accession: JC7568
A:Molecule type: mRNA
A:Residues: 1-298 <LIN>
C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, plays
C:Genetics:
A:Gene: kiap
A:Map position: 20q13.3
C:Keywords: apoptosis

Query Match 45.3%; Score 121; DB 2; Length 298;
Best Local Similarity 45.7%; Pred. No. 2.3e-07;
Matches 21; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46
DB 108 LAAAGFYHTGHQDKYRCFCYGLQSWKRGDDPWEHAKWFPSCOF 153

RESULT 14

T03183
probable apoptosis inhibitor - Chilo iridescent virus
C:Species: Chilo iridescent virus
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Sep-2000
C:Accession: T03183
R:Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A:Reference number: Z14834; MID:98141693; PMID:9482589
A:Accession: T03183
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <BAH>
A:Cross-references: EMBL:AF003534; NID:92738385; PID:AA94481.1; PID:92738454
C:Superfamily: RING finger homology
F:159-202/Domain: RING finger homology <RRN>

Query Match 41.9%; Score 112; DB 2; Length 208;

Best Local Similarity 47.5%; Pred. No. 2.1e-06;
Matches 19; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 40
DB 58 LSRAGFYIUNIGDYQCFCDLKLKWKRSNDNFEHKKH 97

RESULT 15

T43523
cut17 protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000
C:Accession: T43523; T41649; T41700
R:Moriyama, J.; Matsusaka, T.; Yanagida, M.
submitted to the EMBL Data Library, August 1999
A:Description: Fission yeast cut17 is required for chromosome segregation.
A:Reference number: Z22536
A:Accession: T43523
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-997 <MOR>
A:Cross-references: EMBL:AB031034; PID:BA083415.1
R:Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z22007
A:Accession: T41649
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-997 <HAR>
A:Cross-references: EMBL:AL031323; PID:CAA20434.1; GSPDB:GN00065; SPDB:SPCC962.02c
A:Experimental source: strain 972n; cosmid c962
R:Medler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z22010
A:Accession: T41700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 932-997 <WED>
A:Cross-references: EMBL:AL121859; PID:CA058376.1; GSPDB:GN00068; SPDB:SPCP31B10.10c
C:Genetics:
A:Gene: cut17; SPCC962.02c; SPDB:SPCP31B10.10c
A:Map position: 3L
A:Introns: 43/3

Query Match 38.6%; Score 103; DB 2; Length 997;
Best Local Similarity 37.0%; Pred. No. 0.00012;
Matches 20; Conservative 6; Mismatches 20; Indels 8; Gaps 2;

OY 1 LAKAGFY--IGP-----DRVACFACGKLSNWEPRKDNAMSEHLRHPKCP 46
DB 44 LATVGFYINPISSESNSERLDNVTCYMCCKSPFYDWEDDDDPLKEHITHSPSCFW 97

Search completed: May 5, 2003, 16:08:11
Job time : 7.03456 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 15:57:12 ; Search time 11.235 Seconds

(without alignments)
843.627 Million cell updates/sec

Title: US-08-569-749-8

Sequence: 1 LAKAGFYITGPDVACAFAC.....WEPRKNAMSEHLRHPKCP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	235	88.0	374	11	Q921N0 mus musculus
2	232	86.9	589	11	Q9ESE8 rat mus musculus
3	232	86.9	589	11	Q9QZC6 rat mus musculus
4	226	84.6	602	11	Q9ESE9 rat mus musculus
5	223	83.5	195	13	Q9IA70 gallus gallus
6	223	83.5	197	13	Q9IA69 gallus gallus
7	223	83.5	324	13	Q9PDN2 gallus gallus
8	223	83.5	610	13	Q9J319 gallus gallus
9	217	81.3	224	11	Q86642 rat mus musculus
10	195	73.0	628	13	Q8UVD2 brachydanio
11	194	72.7	493	13	Q8UVE8 gallus gallus
12	175	65.5	496	11	Q9ESF0 rat mus musculus
13	175	65.5	501	11	Q9EC05 rat mus musculus
14	175	65.5	501	11	Q9EC04 rat mus musculus
15	152	56.9	403	5	Q8WRD9 oclerolatu
16	145	54.3	236	4	Q96RW5 homo sapien

17	145	54.3	236	4	Q96P09	Q96P09 homo sapien
18	145	54.3	236	6	Q95M72	Q95M72 pan troglod
19	145	54.3	498	5	Q960U3	Q960U3 drosophila
20	144	53.9	236	6	Q95M71	Q95M71 gorilla gor
21	144	53.9	402	5	Q8T621	Q8T621 aedes albop
22	142	53.2	405	13	Q8UWH2	Q8UWH2 brachydanio
23	141	52.8	597	11	Q9R015	Q9R015 mus musculus
24	141	52.8	1160	4	Q8T2D4	Q8T2D4 homo sapien
25	133.5	50.0	153	5	Q9VEM2	Q9VEM2 drosophila
26	131	49.1	106	4	Q96RW6	Q96RW6 homo sapien
27	131	49.1	517	11	Q8R4U8	Q8R4U8 rattus norv
28	130	48.7	264	12	Q9EN27	Q9EN27 amesacta moo
29	129	48.3	438	5	Q9VUX5	Q9VUX5 drosophila
30	127	47.6	346	5	Q968T8	Q968T8 bombyx mori
31	126	47.2	377	5	Q9N707	Q9N707 spodoptera
32	126	47.2	379	5	Q9U492	Q9U492 trichoplusi
33	124	46.4	276	12	Q8Q195	Q8Q195 mamestra co
34	124	46.4	281	12	Q9YNL8	Q9YNL8 choristoneu
35	122.5	45.9	4845	11	Q88738	Q88738 mus musculus
36	121	45.3	261	12	Q9QES9	Q9QES9 epiphyas po
37	121	45.3	280	4	Q9HAP7	Q9HAP7 homo sapien
38	121	45.3	298	4	Q9H2A8	Q9H2A8 homo sapien
39	121	45.3	298	4	Q96CA5	Q96CA5 homo sapien
40	120	44.9	313	12	Q9J827	Q9J827 spodoptera
41	118	44.2	276	12	Q89744	Q89744 buzzard supp
42	116	43.4	268	12	Q9JF18	Q9JF18 helicoverpa
43	116	43.4	268	12	Q9E232	Q9E232 helicoverpa
44	112	41.9	109	6	Q8WMY4	Q8WMY4 bos taurus
45	112	41.9	208	12	Q55770	Q55770 chilio lride

ALIGNMENTS

RESULT 1

Q921N0 ID Q921N0 PRELIMINARY; PRT; 374 AA.

AC Q921N0; 01-DEC-2001 (TREMREL. 19, Created)

DT 01-DEC-2001 (TREMREL. 19, last sequence update)

DT 01-JUN-2002 (TREMREL. 21, last annotation update)

DE Similar to baculoviral IAP repeat-containing 2.

GN BIRC2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strusberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC011338; AA011338.1; -

DR MGD; MGI:1197007; Birc2.

DR InterPro: IPR001370; BIR.

DR Pfam: PF00653; BIR; 3.

DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_3.

DR PROSITE: PS0143; BIR_REPEAT_2; 3.

SQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 88.0%; Score 235; DB 11; Length 374;
Best Local Similarity 89.1%; Pred. NO. 6.9e-23;
Matches 41; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LAKAGFYITGPDVACAFACGKLSNWEPRKNAMSEHLRHPKCP 46
DB 187 LAKAGFYITGPDVACAFACGKLSNWEPRKNAMSEHLRHPKCP 232

RESULT 2
ID Q9ESE8 PRELIMINARY; PRT; 589 AA.
AC Q9ESE8;
DT 01-MAR-2001 (TREMREL. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183431; AAG22971.1; -.
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;
Query Match 86.9%; Score 232; DB 11; Length 589;
Best Local Similarity 84.8%; Pred. No. 2.8e-22;
Matches 39; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
OY 1 LAKAGFYTGPGDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
DB 176 LAKAGFYTGPGDRVACFACGKLSNWEKDNAMSEHLRHPKCP 221
RESULT 3
OY 0902C6 PRELIMINARY; PRT; 589 AA.
AC 0902C6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=KIDNEY;
RC Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF190020; AAF04585.1; -.
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.

KW Zinc-finger.
SQ SEQUENCE 589 AA; 66777 MW; E6812FEE3EA34142 CRC64;
Query Match 86.9%; Score 232; DB 11; Length 589;
Best Local Similarity 84.8%; Pred. No. 2.8e-22;
Matches 39; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
OY 1 LAKAGFYTGPGDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
DB 176 LAKAGFYTGPGDRVACFACGKLSNWEKDNAMSEHLRHPKCP 221
RESULT 4
OY 0902C6 PRELIMINARY; PRT; 602 AA.
AC 0902C6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Inhibitor of apoptosis protein 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183430; AAG22970.1; -.
DR HSSP: Q13490; IQBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 602 AA; 67326 MW; CC91385EBA62DE5A CRC64;
Query Match 84.6%; Score 226; DB 11; Length 602;
Best Local Similarity 82.6%; Pred. No. 1.8e-21;
Matches 38; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY 1 LAKAGFYTGPGDRVACFACGKLSNWEKDNAMSEHLRHPKCP 46
DB 189 LAKAGFYTGPGDRVACFACGKLSNWEKDNAMSEHLRHPKCP 234
RESULT 5
OY 091A70 PRELIMINARY; PRT; 195 AA.
AC 091A70;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE Inhibitor of apoptosis 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BREED LECHORN; TISSUE=SPLEEN;

```
DR InterPro; IPR001315; CARD.  
DR InterPro; IPR001841; Znf_ring
```

DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR Apoptosis; Zinc-finger; Repeat.
FT REPEAT 30 97 BIR_REPEAT 1.
FT REPEAT 176 242 BIR_REPEAT 2.
FT REPEAT 262 329 BIR_REPEAT 3.
FT ZN_FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADF47619650844A6 CRC64;

Query Match 83.5%; Score 223; DB 13; Length 610;
Best Local Similarity 80.4%; Pred. No. 4.5e-21;
Matches 37; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRAVACFACGKLSNWEKDNAMSEHLRHFPCPF 46
DB 196 LAKAGLYLGTADKVACTCGQLSNWEKDNAMSEHLRHFPCPF 241

RESULT 9
ID 088642 PRELIMINARY; PRT; 224 AA.

AC 088642;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein (Fragment).
GN RIAP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-OVARY;
RA Bradley C.K., Lareu R.R., Dharmarajan A.M.;
RT "Cloning and characterisation of an inhibitor of apoptosis protein
RIAP) in the rat corpus luteum."
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
DR HSSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
FT NON_TER 1 1
FT NON_TER 224 224
SQ SEQUENCE 224 AA; 25209 MW; 213A52534D5EB56A CRC64;

Query Match 81.3%; Score 217; DB 11; Length 224;
Best Local Similarity 78.3%; Pred. No. 9.5e-21;
Matches 36; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRAVACFACGKLSNWEKDNAMSEHLRHFPCPF 46
DB 105 LGKAAFYITGPDRAVPCFACGKLSNWEKDNAMSEHLRHFPCPF 150

RESULT 10
ID 08UWD2 PRELIMINARY; PRT; 628 AA.
AC 08UWD2;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE IAP1.
GN IAP1.

OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20373792; PubMed-10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
zebrafish."
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442500; AAL33679.1;
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 73.0%; Score 195; DB 13; Length 628;
Best Local Similarity 69.6%; Pred. No. 2.3e-17;
Matches 32; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRAVACFACGKLSNWEKDNAMSEHLRHFPCPF 46
DB 207 LAKAGLYLGTADKVACTCGQLSNWEKDNAMSEHLRHFPCPF 252

RESULT 11
ID 08UVF8 PRELIMINARY; PRT; 493 AA.

AC 08UVF8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Identification of chicken inhibitor of apoptosis protein XIAP
RIAP3)."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF451854; AAL47170.1;
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match 72.7%; Score 194; DB 13; Length 493;
Best Local Similarity 73.9%; Pred. No. 2,4e-17;
Matches 34; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 LAKAGFYTGPDVACGCGKLSNWEKDNAMSEHLRHFPCPF 46
DB 182 LASAGLYTGVGDVACFCGCGKLNWPCDRAWSEHRRHPCPF 227

RESULT 12

Q9ESF0 PRELIMINARY; PRT; 496 AA.
AC Q9ESF0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183429; AAG22969.1; -.
DR HSSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR ZINC-finger.
KW ZINC-finger.

DR HSSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR ZINC-finger.
KW ZINC-finger.
SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AAEC5B798 CRC64;

Query Match 65.5%; Score 175; DB 11; Length 496;
Best Local Similarity 67.4%; Pred. No. 8e-15;
Matches 31; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

OY 1 LAKAGFYTGPDVACGCGKLSNWEKDNAMSEHLRHFPCPF 46
DB 184 LASAGLYTGVGDVACFCGCGKLNWPCDRAWSEHRRHPCPF 229

RESULT 13

Q9EQ05 PRELIMINARY; PRT; 501 AA.
AC Q9EQ05;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=OVARY;
RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
RT protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF304333; AAG41192.1; -.
DR HSSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.

DR InterPro: IPR001841; Znf_ring.

DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR ZINC-finger.
KW ZINC-finger.

SQ SEQUENCE 501 AA; 56548 MW; 0973F69F2E0C8CD CRC64;

Query Match 65.5%; Score 175; DB 11; Length 501;
Best Local Similarity 67.4%; Pred. No. 8e-15;
Matches 31; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 1 LAKAGFYTGPDVACGCGKLSNWEKDNAMSEHLRHFPCPF 46
DB 184 LASAGLYTGVGDVACFCGCGKLNWPCDRAWSEHRRHPCPF 229

RESULT 14

Q9EQ04 PRELIMINARY; PRT; 501 AA.
AC Q9EQ04;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=OVARY;
RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
RT "Cloning, characterization and regulation of an inhibitor of apoptosis
RT protein in the rat corpus luteum."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF304334; AAG41193.1; -.
DR HSSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR ZINC-finger.
KW ZINC-finger.

SQ SEQUENCE 501 AA; 56578 MW; 4863F69F2E0C8CD CRC64;

Query Match 65.5%; Score 175; DB 11; Length 501;
Best Local Similarity 67.4%; Pred. No. 8e-15;
Matches 31; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

OY 1 LAKAGFYTGPDVACGCGKLSNWEKDNAMSEHLRHFPCPF 46
DB 184 LASAGLYTGVGDVACFCGCGKLNWPCDRAWSEHRRHPCPF 229

RESULT 15

Q8WRD9 PRELIMINARY; PRT; 403 AA.
AC Q8WRD9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 1-like protein.
OS Ochlerotatus triseriatus.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
OC Ochlerotatus.

OX NCBI_TaxID-7162;
RN [1]
RP SEQUENCE FROM N.A.
RA Biltvich B.J., Beatty B.J., Kempf B.J., Mackie R.S., Blair C.D.,
RA Black W.C. IV, Hughes M., Rayms-Keller A.;
RT "Identification and characterization of an inhibitor of apoptosis
RT protein 1 (IAP1) homolog from Aedes triseriatus mosquitoes.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF447592; AAL46972.1; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_1.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 403 AA; 44660 MW; 7765708CB26D6FC2 CRC64;

Query Match 56.9%; Score 152; DB 5; Length 403;
Best Local Similarity 55.6%; Pred. No. 7e-12;
Matches 25; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 1 LAKAGFYIIGPDRAVACFACGKLSNWEPRKNAMSEHLRHFPKCP 45
||:||||:| | | | | :| | | | | :|||| | | |
Db 59 LARYGFYVGPNDMVKCYFCRVEIGLWEPNDNLSEHLRWSPYCP 103

Search completed: May 5, 2003, 16:06:26
Job time : 11.235 secs